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RESULT 15
I47160
Ig gamma 2b
C; Species:
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J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from A;Reference number: 147158; MUID:95015845; PMID:7930579

A;Accession: I47159

A;Status: preliminary; translated from GB/EMBL/DDBJ
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 14715
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C;Genetics:
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A; Residues: 1-328 <KAC>
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chain constant region - pig (fragment)
Sus scrofa domestica (domestic pig)
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                               MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 442
                                                                                                                                                                                                                                                         PSVFLFPKFKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKFREEQYN 324
                                                                                                                                                                                                                                                                                                GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTKTKPPCPICPACESP----G
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                                                                                                                                   LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA
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Pred. No. 1.6e-66;
2; Mismatches 52;
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 (;Accession: I47160 R;KacsKovics, I; Sun, J.; Butler, J.E. J. Immunol. 153, 3565-3573, 1994 A;Title: Five putative subclasses of swine IgG iden: A;Reference number: I47158; MUID:95015845; PMID:7931 A;Accession: I47160 R;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ
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C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-328 <KAC>
A; Cross-references: EMBI
C; Genetics:
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Accession: I47160
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Best Local Similarity
Matches 231; Conserv
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SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK
                                                                                                MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPFVLDSDGSFFLYSKLTVDKS 442
                                                                                                                                                                      STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
                                                                                                                                                                                                                                                                                                                       GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK;3CDKTHTCPPCPAPELLGG 264
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                       RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                         PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY/DGVEVHNAKTKPREEQYN 324
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Search completed: September 12, 2003, 13:04:25 Job time: 37.4831 secs

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A;Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene clon A;Reference number: A02157; MUID:80120716; PMID:6766534
A;Contents: a allele
A;Contents: Contents: Contents:
                                                                                                                                                                                                                                                                                                        A;Introns: 138/1; 236/1; 258/1; 368/1
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap C;Complex: An immunoglobulin cases, such as IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing: duplication; glycoprotein; heterotetramer; immunoglobulin; 157-222/Domain: immunoglobulin homology <IM1>
F;336-257/Region: hinge
F;381-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;144-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A:Cross-references: GB:J00461
R:Kim, H: Yamaguchi, Y: Masuda, K: Matsunaga, C:; Yamamoto, K:; Irimura, T:; Ta
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A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210;
A:Yamawaki-Kataoka, Y.; Kataoka,
Nature 283, 786-789, 1980
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A;Molecule type: protein
A;Residues: 234-251 <KIM>C;Comment: The a allele sequence is shown.
C;Genetics:
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Best Local
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                                                                                                                                                                                                                                   Similarity
GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE
                                                                                                                                            MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                      MEWSWIFLFLLSGTAGVHSEVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKP
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                                                                                                                                                                                                                                   Score 1417; DB 1;
Pred. No. 4.8e-75;
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A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;NOte: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;2-1-19/Product: Ig gamma-2b chain #status predicted <MAT>
F;159-223/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Expression A; Reference number: A; Accession: S01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fier
Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphoid cells of mouse recombinant
A;Reference number: S01320; MUID:88329081; PMID:3138116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig gamma-2b chain precursor - mouse C: Species: Mus musculus (house mouse) C: Date: 30-Sep-1989 #sequence_revision C: Accession: S01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-475 <DE1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
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                                                                                                                                                                                              VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 180
                                                                                                                                                                                                                                                                                                        VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                                                                                           GQGLEWIGETYPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQ
                                                                                                                                                                                                                                                                                                                                                                                    MEWIWIFLFILSGTAGVQSQVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRT
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RVEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                      VTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDK
                                                                                                                                                                  VGLL----PFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55.7%; Score 1401.5;
55.3%; Pred. No. 3.86
Live 82; Mismatches
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3.8e-74;
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R.Khamlichi, A.A.

R.Khamlichi, A.A.

submitted to the EMBL Data Library, September A:Reference number: $72664
                                                          RESULT
S40295
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If heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Blochem. 229, 54-60, 1995
Eur. J. Structure of abnormal heavy chains in human heavy-chain-deposition
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision
C;Accession: S40295
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A; Residues: 1-140, 'C', 142-374 <KH2>
A; Cross references: EMBL: X81695
C; Superfamily: immunoglobulin C region;
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A; Residues: 1-374 < KHA>
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                                                                                                                                                                        KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG
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                                                                                                                                                GK 474
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                                                                                                                                                                                                                                                                                                            VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                                                                                                                                                                                                                                                                                                                                                    PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
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                                                                                                                                                                                                                                                                                             VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
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                                                                                                                                                                                                                                                                                                                                                      -EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYGQGYRFHSWGQGTLVTVSS---
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          07-Apr-1994 #text_change 16-Jul-1999
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RESULT 12 G2MS11

Ig gamma-2b chain - mouse C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Caccession: S25057; A02157; A26235; A26232; A26233; A33598 R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzale submitted to the EMBL Data Library, July 1992 submitted to the EMBL Data Library, July 1992 A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neoto

A; Reference number: A; Accession: S25057

S25057

inactivating neotop H.J.; Kreuzaler,

specifi

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R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgert submitted to the EMBL Data Library, January 1993

A;Description: Primary structure of the murine monoclon:1 IgG2a antibody mAb7:
A;Reference number: $40295

A;Reference number: $40295

A;Reference number: $40295

A;Recession: $40295

A;Recession: $40295

A;Recicule type: protein
A;Residues: 1-446 <KLE>
C;Genetics:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin Domology
C;Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
E;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: Cy region <CHP>
F;1-117/Domain: Cr region <CHP>
F;1-18-244/Domain: Cr region <CHP>
F;218-240/Domain: Cr region <CHP>
F;318-240/Domain: Cr region <CHP>
F;31-340/Domain: Cy region <CHP>
F;31-340/Domain: Cy region <CHP>
F;31-340/Domain: Cy region <CHP>
F;31-340/Domain: Cy region <CHP>
F;1-1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;32-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;32-1,729/Disulfide bonds: interchain (to light chain) #status predicted
F;24,27,229/Disulfide bonds: interchain #status predicted
F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                          EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAFGKGLEWVSAISASGHSTYL
RVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                                                                                          THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYV
                                                                                                                                                                                                                                      VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRFGEGLEWIGWIYPGSGNTKY
                                      TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                               PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPANIEKTISKAKGQPREPQVYT
                                                                                                                                                                                                                                                                                                                       VLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDRKIEPRG-PTIKPCPPCKCP
                                                                                                                                                                                                                                                                                                                                                VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDLRVEPKSCDKTHTCPP--CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAM-----
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                                                                                                                                                                                                                                                                                                                                                                                                       VTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEIVTLTWNSGSLSSGVHTFPA
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353 358 293

413

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S37483
S37483
Ig gamma-2a chain -
C:Species: Mus musc
C:Date: 06-Jan-1995
C:Accession: S377483
R:Ducancel, F.F.D.
                                                                                                                                                                                                                                     submitted to the EMBL Data Library, February 1993
A; Reference number: $37483
A; Accession: $37483
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-469 < LOUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin C:Keywords: immunoglobulin C:Keywords: immunoglobulin C:Keywords: immunoglobulin homology < CMM>
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;Species: Mus musculus (house mouse)
;Date: 06-Jan-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                          Accession: S37483
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Best Local :
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hes 281;
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                                                 VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
                                                                                    NGGF-DYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGIT-SGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARS---TYGEVG
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                                       ATATLL ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDVEVNTATTKPREEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFVLSAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGPAREPQVYVLAPPQEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQ
                                                                                                                                                                                       Conservative
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                                      -DYWGQGTTLTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEP
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62.1%;
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                                                                                                                                                                                                Score 1482.5; DB Pred. No. 7.6e-79;
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Pred. No. 9.6e-80;
1; Mismatches 107;
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                                                                                                                                                                                       104;
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$31459
Ig gamma-1 chain - sheep (fragment)
C; Species: Ovis orientalis aries, Ovis am
C; Date: 13-Jan-1995 #sequence_revision 13
C; Accession: $31459
R; Patri, S.; Nau, F.
submitted to the EMBL Data Library, Decer
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C r
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin
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A; Residues: 1-472 < PAT>
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A; Accession: S31459
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                          TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                           RVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                                                                                                            SWFYDNYEYRTARTKPREEQFNSTFRYVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRT
                                                                                                                        NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                             SHAFAYASYDFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVT
                                                                                                                                                                                                                                                                                                                                    SAISASGHSTYLAD-----SVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVT
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              TTSQLDADGSYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK
                                                                         ISKAKGQPREPQYYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT
                                                                                                                                                                        EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                             EPGCPDPCKHC-RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQF
                                                                                                                                                                                                                                                                                                             -----GGSGYDEDIDYNPVLKSRLSITKDTSKSQVSLTLSTVTTEDTAVYYCARVDYDS
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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58.9%;
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13-Jan-1995
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#text_change
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358

239

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A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14932.33-14922.33

A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical ligh c;Complex: An immunoglobulin c region; immunoglobulin homology

C;Superfamily: immunoglobulin c region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;140/Disulfide bonds: interchain (to light chain) #status experimental

F;27-83,141-201.247-305/Disulfide bonds: #status predicted

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A90933
A;Molecule type: DMA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Pa A;Reference number: A90249; MUID:70207560; PMA;Accession: A90249
                                                                 RESULT 6
PC4436

MCDACCESSION: PC4436

R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M. Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A; Title: Structural characterization of mouse monoclonal antibody 13-1 agair A; Reference number: JC5810; MUID: 98063277; PMID: 9398605

A; Accession: PC4436

A; Accession: PC4436
     A; Molecule type: protein A; Residues: 1-444 <AKA> C; Comment: This catalytic C; Superfamily: immunoglok
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLYSLSSVYTYPSSSLGTQTYICNVNHKPSNTKYDKRVEPKSCDKTHTCPPCPAPELLGG
                                                                                                                                                                                                                                                                                                            QEGNVFSCSVMHEALHNHYTQKSLSLSLGK
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   immunoglobulin C region;
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Pred. No. 8.4e
9; Mismatches
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A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL: X16701
A; Note: the sequence was determined from the germl C; Genetics:
A; Gene: Ig CH gamma-1
A; Introns: 98/1; 111/1; 221/1
C; Superfamily: immunoglobulin C region; immunoglob C; Keywords: 91ycoprotein; heterotetramer; immunogl F; 161-225/Domain: immunoglobulin homology <IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                         A;Cross-references: EMBL:X62916; NID:g439; F R;Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin A;Reference number: S06610; MUID:90097956; P A;Accession: S06610
                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine N;Alternate names: Ig gamma-1 chain C region (clone C;Species: Bos primigenius taurus (cattle) C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #c;Accession: $22080; $06610; A31303
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A; Residues: 1-470 <SAN>
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F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:134/Disulfide bonds: interchain (to light chain) #status experimental F:27-83,140-200,246-304/Disulfide bonds: #status experimental F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IMIX.
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A; Residues: 238-275 <HOFS
R; Hofmann, T.; Parr, D.M.
submitted to the Atlas, March
A; Reference number: A94591
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Biochem. J. 121, 217-225, 1971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L. Nature 221, 145-148, 1969
В
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QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 326
                                      QQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                   MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPMLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                          MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW
                                                                                                                                                                                                                                                                                                  STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE
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RESULT 5

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Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text

C;Accession: A90933; A90249; A02150

R;Ellison, J.; Buxbaum, J.; Hood, L.

DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin CA;Reference number: A90933; MUID:83157104; PMID:6299662

#text_change

16-Jul-1999

C-gamma4

gene

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A;Reference number: A'A;Contents: myeloma p
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A; Residues: 1-96, 'R', '98-197,'D', 199-238,'E', 240,'M', 242-266,'D', 268-271,'D', 273-330
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Blochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu
A; Reference number: A90565; MUID:71064027; PMID:4923144
A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1518-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immuno enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070267; PMID:1002129
A; Contents: annotation; disulfide bonds
C; Generics:
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A;Molecule type: protein
A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',A;Note: this sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Prinaerstruktur des kristallsierbaren monoklonalen Immunglobulins IgG1 1
A;Reference number: A91723; MUID:83289131; PMID:6884994
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99.1%;
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Pred. No. 5.5e-95;
3; Mismatches 0;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
C;Superfamily: immunoglobulin C
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin
                                                                                      R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele (Gmb0, bl, A;Reference number: A60764; MUID:90007613; PMID:2571587
A;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy cha A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CA
                                                                                                                                                                 Ig gamma-3 chain C region, form LAT - | C;Species: Homo sapiens (man) C;Date: 14-May-1993 #sequence_revision C;Accession: A60764
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A60764
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 14:
C;Superfamily: immunoglobulin C re
C;Keywords: immunoglobulin
F;20-85/Domain: immunoglobulin hon
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A;Gene: GDB:IGHG3
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7; Mismatches
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Listing first 45 summaries
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ALIGNMENTS

RESULT

A; Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni	Ig gamma-3 chain C
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A; NOTE: THIS SEQUENCE HAS THE GAMMAND AND MALES, 255 GAMMAND AND THE GAMMAND THE GAMMAND AND THE GAMMAND AND THE GAMMAND AND THE GAMMAND AND	Ig gamma-2b chain
A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-194, 'U', 199-238, 'E', 2	
A; Molecule type: protein	Ig gamma-1 chain C
A;Accession: A90564	
A; Contents: Eu	
A; Reference number: A90564; MUID: 71064025; PMID: 5530842	gamma-2 chain
A; Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se	gamma 3 chain
Biochemistry 9, 3171-3181, 1970	gamma chain C
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.	gamma 1 chain
A; Note: this sequence has the Glm(3) marker, 97-Arg	
A; Residues: 1-96, 'R', 98-135 <cun></cun>	
A; Molecule type: protein	qamma
A; Accession: B90563	
64024; PMID:5489771	
of a human	
R:Cunningham B A : Rufishauser II : Gall W E : Gottleeb P.D.: Waxdal M.J.: Edelma	
A: Cross references: EMRI: 27 7370	Ig gamma-2a chain
A: Residines: 88-113: 735-330 <tak></tak>	Ig heavy chain pre
A.MOIDOILE TUNE DIA	monoclonal antibod
A.A.C.D.G.G.J.G.R.G.J.G.G.R.G.L.G.G.G.G.G.G.G.G.G.G.G.G.G.G.G	gamma-4 chain
PMID: 6811139	gamma - 2 chain
A. Title of the contract of human immunocal challen gamma gapage implications for evolution of	gamma - 3
R, Landing HL, N., Octob, G., Obeco, N., Minateo, J., Manati, J., Monijo, J.	Chain
۵	ramma - 1
A; RESIQUES: 2-350 <hak></hak>	Description
A; Molecule type: DNA	
A;Accession: S36861	
submitted to the EMBL Data Library, October 1992	
R; Harris, L.J.	distribution.
	result
A: Note: this sequence has the Glm(17) allotypic marker, 97-Lvs, and the Glm(1) marker	v chance to have a
A; RESIQUES: 1-330 <ell></ell>	
A; MoLecule type: DNA	
A;Accession: A93433	
A; Reference number: A93433; MUID:82274238; PMID:6287432	
A; Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.	
Nucleic Acids Res. 10, 4071-4079, 1982	
R.E. lison. J. W. Berson B. T. Hood. I.	
C:pate: 31-Jan-1981 #sequence_revision 18-Aug-1992 #fext_change 10-Jul-1999 C:nocose:jon. Agg143: <33887: Agg187: Agg188: Agg188: Agg173: Agg188: Agg1	
C; Species: Homo sapiens (man)	
Ig gamma-1 chain C region - human	
GHHU	
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RESULT 15
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New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of this sequence, the complementarity determining regions (CDRs) coriginates from murine monoclonal antibody 3D6 and the framework region originates from human germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibodies, The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of a preferred heavy chain of a humanised antibody of the present invention. In the variable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                              DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                          EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379
                                                                                                                                                                                        VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259
                                                                                                                                                                                                                                                                                                                                        VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199
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                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFDYWGQGTR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVQLLESGGGLVQPGGSLRLSCAASGFTESNYAMSWVRQAPGKGLEWVSAISASGHSTYL
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89.1%; Score 2241; DB 24; 92.3%; Pred. No. 3.7e-132; tive 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English
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Search completed: September 12, 2003, 13:00:39 Job time: 83.0085 secs

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, is also useful for treating osteopenic disorder, an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a patient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, wenkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and osteonecrosis
   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                      Sequence
                                          25-MAR-2003
28-DEC-1992
                                                                          AAR24812;
                                                                                             AAR24812 standard; Protein; 466
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                                                                                                                                               TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBGK 474
                                                                                                                                                                                                                                VTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                                                                                                                                                                           TTVIM----SWFDPWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                                                                     GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE 120
                                                                                                                                                                                                  KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                                                                                            TVERKCCVE--
                                                                                                                                                                                                                                                                                   RVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
                      encoded by the chimeric H chain cDNA contained in
                                                                                                                                                                                        KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                   GKGLEWVSGITGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                            MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                        (first entry)
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 antibody;
                                                                                                                                                                                                                                                                          -CPPCPAPP-VAGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEV
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Pred. No. 2.3e-132;
anti-fibrin antibody; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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chimeric anti-human firbrin heavy chain cDNA open reading chimeric anti-human firbrin heavy chain cDNA open reading chimeric Ab-producing transformant FIB1-HO1/X63 as a template to clone human C-kappa cDNA, using the oligo-dT (Fharmacia) primer as a primer for first strand cDNA synthesis and the 5'C2H and 3'EH cprimers for the PCR. A human gamma-1 chain CH2-CH3 domaine encoding cDNA was amplified. Similarly a human gamma-1 chain CH1 domain encoding cDNA and an anti-fibrin antibody VH cDNA and a leader peptide cDNA were amplified using the primers 3'EH; 3'C2H and 3'CH respectively as a primer for first strand cDNA synthesis and the primer combination of 5'C1H and 3'C2H, of 5'LH and 3'C1H and of 5'SH and 3'LH respectively as a primer for FCR. The amplified gene products were isolated and used to produce plasmids. After confirmation of the cDNA sequence of each plasmid, the cDNA encoding LH, VH, CH1 and CH2CH3 were joined toge!ther to give plasmid pTB1373 contg. the whole length chimeric II chain (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FII,
    Query Match
Best Local S
Matches 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example; Figure 11; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD
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11-NOV-1991;
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    hes 424;
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                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pTB1373 contains the whole length of a mouse-human
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    Conservative
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91JP-0294464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= VH
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'= CH1
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                    89.3%;
    18;
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Score 2244; DB 13;
Pred. No. 2.5e-132;
8; Mismatches 22;
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      Indels
                                              Length
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mediated immunological or inflammatory disorders such as skin related conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal conditions (e.g. ripintal conditions (e.g. kidney or lung cibrosis), allergic rinintis, respiratory distress syndrome, asthma, concentritis, tendonitis, bursitis, fever, migraine headaches, gastro-concentritis, tendonitis, bursitis, fever, migraine headaches, gastro-contestinal conditions (e.g. inflammatory bowel disease, Crohn's disease, castritis, irritable bowel syndrome, colitis and colorectal cancer), cascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, periartic anticolorectal cancer (e.g. type I diabetes, myasthenia gravis, rheumatoid carthritis, systemic lupus erythematosus and multiple sclerosis), renal carthritis, systemic lupus erythematosus and multiple sclerosis, gingivitis, polymyositis, hypersensitivity (e.g. delayed type hypersensitivity or inmediate hypersensitivity), graft and transplant rejections, graft
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; very late activation antigen; VLA-1; betal containing integrin; Immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bristitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behcet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia.
                                                         Sequence
                                                                                           versus host disease, conjunctivitis, swemyocardial ischaemia or endotoxin shock is human AQC2 heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The anti-VLA-1 antibodies are useful for preventing or treating VLA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-APR-2001; 2001US-283794P
06-JUL-2001; 2001US-303689P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Page 75; 248pp; English.
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                                                           447
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93
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. 38;
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Score 2244.5; DB 2
Pred. No. 2.2e-132;
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                                                                                                         swelling occurring after injury, ock syndrome. The present sequence
                 24;
                 Length 447;
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RESULT 13
ABP71365
ID ABP71367
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XX ABP71
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XX OStec
KW OSTEC
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WPI; 2003-210262/20
N-PSDB; ABZ59147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Osteoprotegerin ligand; osteopathic; antlinflammatory; antirheumatic; antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.
                                                                                                                                            (ABGE-)
                                                                                                                                                                                                                                   26-JUN-2001; 2001US-301172P
                                                                                                                                                                                                                                                                                                                                                  09-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
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                                                                                       Boyle WJ,
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                                                                                                                                            ABGENIX INC.
AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSK
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                                                                                    Martin FH,
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/note= "variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "IgG2 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                    Corvalan
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "constant region"
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                                                                                       JR,
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436

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RESULT 11
AAE34876
ID AAE34
XX AAE34
AC AAE34
XX 28-M2
XX 28-M2
XX BIWA4
XX BIWA4
XX BIWA6
XX WH; N
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antigen
DNA enco
                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences (AAO54651-52) show the light and heavy chain cDNAs of murine T84.12. The T84.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for tumour imaging and immunotherapy. The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'. The amino acid sequence given below has been derived from the cDNA, by the indexer.

(Updated on 25-MAR-2003 to correct PN field.)
              Unidentified
                                                                   28-MAY-2003
                                                                                  AAE34876
                                                                                                AAE34876
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                             antibody;
L; CD44v6;
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                                                    antibody
                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                             TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                 KTISKAKGQPREPQYYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                    TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                         EKRLEWVASISSDG-ITFYVDSVKGRFTVSRDNARNILYLQMSSLRSEDTAMYYCAR---
                                                                                                                                                                                                                                                                                                                                                       MNFGFSLIFLVLVLKGVQCEVKLVESGGGFVKPGGSLKLSCAASGFTFSSYAMSWVRQTP
                                                                                                                                                                                                                                                                                                                                                                                                                    477
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                c T84.12 antibody active against carcinoembryonic s murine variable and human constant regions, also it and transformed myeloma cells
                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-23; 27pp; English.
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                            heavy chain medicament;
                                                   heavy chain
                                                                                                Protein;
                                                                 entry)
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                                                                                                444
                            variable region; light chain cancer; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                            Score 2257;
Pred. No. 3.
                                                   mature
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Query Match
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Matches 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies CD44 gene, usef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Van Dongen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adolf G,
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26-SEP-2001;
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DB; AAD53212, AJ
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BOEHRINGER
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                                                                                                                                                                                                                                                                                                                        EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQA;GKGLEWVSAISASGHSTYL 79
                                                                                                                                                                                         VLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                                         DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                             PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYY.TTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGEDYWGQGTR 139
                                                                                                                                              EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPJEKTISKAKGQPREPQVYTLP
                                                              PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYI:TTPPVLDSDGSFFLYSKLTV
                                                                                                                             EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP) EKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQA?GKGLEWVSTISSGGSYTYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        444 AA;
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2001US-325147P
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92.7%;
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PHARM INC
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The invention describes an isolated mucin-1-specific binding member having an antigen binding domain including a region that comprises a specific amino acid sequence. The inventive MUC1-specific binding member is used in the diagnosis and/or treatment of cancer, e.g. adenocarcinoma, found in various tissues, e.g. breast, ovary, bladder, and lung. It can be used alone or as a component in a more complex anti-cancer regimen which may contain anti-cancer drug(s) and/or radiation treatment(s). The inventive binding member recognizes tumour-associated MUC1 on adenocarcinoma. Its affinity is high enough to bind to tumour cells. This is the amino acid sequence of a mucin 1 (MUC-1) specific antibody region used to isolate MUC-1 antigen binding domains for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mucin-1-specific binding member; human; cancer; adenocarcinoma; breast cancer; ovarian cancer; bladder cancer; lung cancer; anti-cancer regimen; anti-cancer drug; radiation treatment.
                                                                                                                                                                                                                                                                                                                              Claim 12; Page 41-42;
                                                                                                                                                                                                                                                                                                                                                                         Isolated mucin-1-specific binding member for diagnosing and/or treating
cancer, e.g. breast cancer, comprises antigen binding domain having
region that contains specific amino acid sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-198057/19.
N-PSDB; ABX79100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HEND/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABU58807 standard; Protein; 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoogenboom HRJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAR-2001; 2001US-0822698.
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HENDERIKX M P G.
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        WPI; 1994-007204/01.
N-PSDB; AAQ54655.
                                                                                      Fischer R,
Yang YH;
                                                                                                                                                               (CITY ) CITY (YANG/) YANG
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24-JUN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     c; carcinoembryonic
transform; myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISASGHSTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYS
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(first en
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93.2%;
                                                                                                              Shively JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen; CCA; murine; mouse;
cell; light chain; tumour.
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Pred. No. 3.7e-133;
7; Mismatches 12;
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Yang YHJ;

constant;

DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

449

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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the heavy chain variable region of a rat immunoglobulin G (IgG) antibody which is specific for the CD3 antigen complex, and the human CH1-hinge-aglycosylCH2CH3. The specification describes chimeric human/rodent anti-CD3 antibodies, which have a rodent CD3 light chain variable region and a human heavy chain variable region. The anti-CD3 antibodies can render T-cells non-functional by antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex. They can be used for immunosuppression, particularly for the control of graft rejection. The antibodies can also enhance or re-direct T-cell responses to antigens. They can be used in the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New humanized anti-CD3 antibodies, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppression and preventing
                                                                                                                                                                                                                                                                                                                                                                         Local
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                                 VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                   VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199
                                                                                                                                                                                                                                                                                                                           EVQLLESGGGLVQPGGSLRLSCAASGETESNYAMSWVRQAPGKGLEWVSAISASGHSTYL 79
                                                                                            EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                         ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                                                                DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                             ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                            VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                       VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                                                                EEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                            449
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 45-47;
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                                                                                                                                                                                                                                                                                                                                                            Score 2279; D)
Pred. No. 1.5e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   graft rejection
                                                                                                                                                                                                                                                                                                                                                                         DB 21;
.5e-134;
                                                                                                                                                                                                                                                                                                                                                                                  Length 449;
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QY DB QY DB QY QY

QGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH

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RESULT 8
AAE12715
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                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                   Query Match
Best Local :
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heavy chain region; cancer; breast; ovary; lung; bladder;
cytostatic; therapy; immunoglobulin; Ig.
                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 106-108; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated tumor-associated antigen mucin-1-specific binding member for diagnosing and treating cancer, comprises mucin-1 binding domain or its portion for binding to an epitope of the protein core of mucin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-626437/72
)B; AAD20745.
                                                                                                                                                                                                                                       428;
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                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                              EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQLPGKGLEWVSAISASGHSTYL
                        ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDI:EVTMIVVLNGG----FDYWG
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                                                                                                               QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQI.PGKGLEWVSGISGSGGSTYY
ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKH…----TGGGVWDPIDYWG
                                                                                                                                                                                                                                                                                                                                                          451 AA;
                                                                                                                                                                                                                                       Conservative
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93.2%;
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                                                                                                                                                                                                                                                             Score 2257; DB 22; Pred. No. 3.7e-133;
                                                                                                                                                                                                                                       Mismatches
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RESULT 6
AAU07745
ID AAUC
XX AAUC
XX O4-E
AC AAUC
DT 04-E
XX Huma
XX Man
KW Alzh
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PR 26-E
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08-DEC-2000; 2000US-0254465
08-DEC-2000; 2000US-0254498
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanised monoclonal antibody Hu266, heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU07745
  Holtzman
                                               (UNIW ) UNIV WASHINGTON (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                   26-FEB-2001; 2001WO-US06191
                                                                                                                                                                                                                                                                                                                 WO200162801-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monoclonal antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTMIVVLNGG-----FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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  Demattos R,
                                                                                                                                                                                                                                                                                                                                                           /label= Mature_Hu266_heavy_chain
/note= "This sequence is specifically claimed
claim 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..19
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal_peptide
20..461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hu266; nootropic; neuroprotective; Abeta peptide;
Down's syndrome; cerebral amyloid angiopathy;
  Bales
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  KR,
  Paul
  , MS
  Tsurushita
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RESULT 7
AAY68810
ID AAY6
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AC AAY6
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AAY68810 standard;

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AAY68810; 16-MAY-2000

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antibody; immunosuppression; heavy chain;

CD3 antigen complex; chimeric

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre-clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanised antibody for the treatment of Alzheimer's comprises inhibition and reduction of the formation of amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vasquez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates a humanised antibody that specifically binds
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                                                           348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Fig 5; 63pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                      VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                          KTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKT
                                                                                                                    VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 180
------DYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 167
                                                                                                                                                                                                                                                                                                                                                          GKGLELVAQINSVGNSTYYPDTVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCASG--
                                                                                                                                                                                                                                                                                                                                                                      GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE 120
                                                                                                                                                                                                                                                                                                                                                                                                                    MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       461
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A
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91.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2304.5; DB 2
Pred. No. 4.1e-136;
3; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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WO200288306-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of a preferred heavy chain of a chumanised antibody of the present invention. In the variable region of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline VH segment DP-45 and J segment JH4. Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical angiopathy, and to inhibit formation or reduce Abeta plaque in the brain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 434
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                                                                                                                           KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                                                    VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YSGSSDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKGLEWVASIRSGGGRTYYSDNVKGRFTISRENAKNSLYLQMNSLRAEDTAVYYCVRYDH
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2002WO-US11853
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91.6%;
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Pred. No. 9.1e-137;
6; Mismatches 18;
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RESULT 5
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Query Match
Best Local Similarity
                                              The variable region of the heavy chain is upprotein with the variable region from the kithe two V regions being joined by a linker. binds to HIV gp160.
                                                                                                Recombinant protein which binds to complex viral antigen a HIV-1 - contains variable region of antibody derived from cell line, used for detecting HIV-1 antigen
                                                                                                                                                                                                                                                                                                                                   Region
                       Sequence
                                                                                    Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR20057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR20057
                                      See also
                                                                                                                                                      Felgenhauer M,
                                                                                                                                                                    (JUNG/) JUNGBAUER A.
                                                                                                                                                                                    29-MAY-1990;
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                                                                                                                                                                                                                  12-DEC-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                     complementarity
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                                                                                  Page 24; 52pp; German.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein;
                       475
                                                                                                                                                                                                                                                                                                                                                                                                                                            of 3D6 anti-HIV antibody
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                                                                                                                                                                                                                                                                Framework_4
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Score 2309.5; DE Pred. No. 2e-136;
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RESULT 3
AAU14288
AID 14288
AID 1428
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                                                                                                                                                                                                                                                                                                                                    The invention relates to polynucleotides encoding novel human CC proteins or their active domains. The polypeptides, polynucleotides and CC antibodies raised against the polypeptides are used in a method of CC treatment of a mammal and prevention of disorders caused by the aberrant CC protein expression or activity. The polypeptides can be used as CC molecular weight markers, food supplements, and in antibody production. CC The polypeptides are used to identify compounds which bind to the CC polypeptides. Polynucleotides of the invention are used as probes and CC primers, for sequencing, for chromosome or gene mapping, in the CC production of recombinant proteins, and in generating anti-sense DNA or CC RNA and in gene therapy. Polypeptides of the invention can be used to CC target drugs to a tumour, in assays to determine biological activity, to CC raise antibodies/elicit an immune response, to determine quantitative CC protein levels, as tissue markers, and to isolate receptors or ligands. CC Polypeptides of the invention may also be useful in treating platelet CC ligament and/or nerve tissue, wound healing, treating borns, promoting the part of the nortiferartion can be defermed and considers.
                                                                                                    fungal infection or from autoimmunity, cancer, allergy, asthma,
graft-versus-host disease, eczema, haemophilia, thrombosis,
anti-inflammatory diseases, nervous system disorders, and infec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
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       Sequence
                                                                                                                                                                                                      the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lat sclerosis, stroke, immune deficiencies resulting from bacterial, vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2001
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                                                                        present sequence
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Best Local Similarity
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Peptide
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No. 4.9e-139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monoclonal rables virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for treating an individual exposed to a rables virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rables virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious p
                  Human; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rables; neurological disease; infection; central nervous system; rables virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; heavy chain.
                                                                                                                                                                                                      10-MAY-2003
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                                                                                                                                                                                                                                                                                                      ABU08017 standard;
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cing spread of rabies virus to central nervous system -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
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CC The invention discloses a recombinant antibody comprising a constant CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable CC region. Rabies is an acute, neurological disease caused by infection of CC the central nervous system with the rabies virus, a member of the CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods CC for producing an isolated recombinant antibody by culturing a host cell, CC containing a recombinant expression vector comprising the nucleic acid CC molecule encoding the antibody, and isolating the recombinant antibody CC expressed and treating an individual exposed to a pathogen by administering to the individual the recombinant antibody. The recombinant CC expressed to a pathogen, e.g. rabies infection. They are also useful for the qualitative and quantitative determination of the rables virus. The CC sequences presented are the antibody protein fragments, the nucleic acids CC encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 200
N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                 New recombinant antibody comprising a constant region to a non-Mab 57 variable region, useful for treating a exposed to a pathogen, e.g. rables infection
Sequence
                                    expression
                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 32-33; 38pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYJE-) UNIV JEFFERSON THOMAS
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                                    vector.
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Query Match 100.0%; Score 2514; DB 24; Length 474; Best Local Similarity 100.0%; Pred. No. 3.4e-149; Matches 474; Conservative 0; Mismatches 0; Indels 0; Gaps 0

, Db Qy Q Qy δÃ QY 밁 Qy 망 Q 밁 밁 멍 멍 361 361 301 301 241181 181 121 121 61 61 ш \vdash KTISKAKGQPREPQYYTLPPSREEMTKNQVSLTCLVKGFY)'SDIAVEWESNGQPENNYKT RVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI:RTPEVTCVVVDVSHEDPEV VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL(:TQTYICNVNHKPSNTKVDK VTMIVVLNGGEDYWGQGTRVTVSSASTKGPSVFPLAPSSK%TSGGTAALGCLVKDYFPEP GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYL(MNSLRAEDTAVYYCAKDRE MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSC AASGFTFSNY AMSWVRQAP GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYL(:MNSLRAEDTAVYYCAKDRE MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLS(AASGFTFSNYAMSWVRQAP VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSK!/TSGGTAALGCLVKDYFPEP 240 180 120 420 420 360 120 60 360 300 240 180 300

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Title:
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                                              2514
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Gapop 10.0 , Gapext 0.5
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2514
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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                    AAO14065
ABU08017
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AAR20057
AAU07745
AAY68810
AAE12715
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Human novel protei
Humanised 3D6 anti
Heavy chain of 3D6
                                                                                                                                                                                                                         Description
                                       Humanised monoclon
A rat heavy chain
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2183	2183	2184.5	2187	2187.5	2188	2193.5	2193.5	2193.5	2193.5	2193.5	2196	2196	2218.5	2219	2220	2221	2221	2221.5	2226.5	2226.5	2226.5	2232.5	N	2235	2237.5	2237.5	2237.5	2238	2238.5	2241	2244	244.	2244.5	249.	2257
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23	19	19	23	23	23	24	24	21	21	20	24	23	23	23	22	23	23	14	24	24	24	23	24	23	24	24	24	23	24	24	13	24	24	24	15
AAU11644	AAW63763	AAW69316	ABB81110	ABG77162	ABG77161	ABU13799	ABU59512	AAY77766	AAB30322	AAY29458	ABP72748	ABB81109	AAU81993	ABG77157	AAB81987	ABG78151	ABG91842	AAR42066	ABU08320	ABR39474	ABB80113	AAO18400	AAE33524	АВJ10365	ABU08311	ABR39465	ABB80109	ABG77158	AAE33523	ABP58273	AAR24812	ABP71365	AAE33522	œ	AAR47453
	Macaque primatized	Anti-IL-8 humanise	Anti-VEGF heavy ch	Germline protein s	Amino acid sequenc	Humanised mouse an	Humanised Mouse an	Humanised anti-IL-	Humanised anti-IL-	Recombinant immuno	tissue		Human secreted pro	Amino acid sequenc	Ganglioside GD3 sp	Human Fv molecule	Human antibody fra		Humanised antibody	Humanised anti-Abe	Deglycosylated hea			asts		Ľ	Heavy chain. Homo		Human AQC2 heavy c		Sequence encoded b	l antik	AQC2 }	=	chiT84.12 H3 heavy

ALIGNMENTS

RESULT 1
AAO14065
ID AAO1
XX AAO1
XX AAO2
DT 07-1
XX Hea
XX Hea
XX Huri
KW Hri
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KW huri
KW huri
XX Hor
XX H HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain; human monoclonal rabies virus neutralising antibody; immunoglobulin; light chain; central nervous system; CNS; prophylactic therapy; clone JA. Hooper DC, (UYJE-) UNIV JEFFERSON THOMAS 16-MAY-2000; 2000US-204518P. 04-MAY-2001; 2001WO-US14468 22-NOV-2001 WO200188132-A2 Homo sapiens. Heavy chain protein of the monoclonal antibody from clone 07-MAY-2002 AAO14065; AAO14065 standard; Protein; 474 Dietzschold (first entry) ₽; ₽ JA

1 (MUC-1)

WPI; 2002-062381/08. N-PSDB; AAK98701.

Novel isolated human monoclonal rabies virus neutralising antibody

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Result
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Maximum
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length: 2000000000
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0 /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
1 /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
1 /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
2 /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
3 /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
4 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
5 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
6 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
7 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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US-09-848-32-4
US-10-153-382-7
US-10-153-382-15
US-10-153-382-11
US-09-859-053-38
US-09-859-053-38
US-09-453-234-88
US-09-453-234-86
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US-10-225-108A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10225108A Publication No. US20030157112A1
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: HOOPER, Craig
APPLICANT: HOOPER, Craig
TITLE OR INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4
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•	Sequence 38, Appl	•	40	Sequence 78, Appl	44	4	Sequence 69, Appl	42	Sequence 52, Appl	38	55	Sequence 36, Appl	Sequence 80, Appl	50	22	10	Sequence 54, Appl	, 88	118	74,	Sequence 47, Appl	127	52	Sequence 24, Appl	13	12	5	1,	Sequence 50, Appl

ALIGNMENTS

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; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-4
                                                                              Matches
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Best Local (
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nes 234; Conserv
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        61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLE; PEDFAVYYCQQRFNWPWTFGQ 120
                                     Conservative
                                                                                        100.0%;
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                                                                            Score 1223; DB 12.
Pred. No. 1.2e-72;
Mismatches 0;
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                                                                                                 Length
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; TYPE: PRT
; ORGANISM: Homo
US-10-153-382-7
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US-10-153-382-7
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                                                                                                                                                  Sequence 7, Application US/10153382
Publication No. US20030086930A1
GEMERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TIFLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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   Query
                                                                                                     SEQ ID NO 7
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
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APPLICANT: Dietzschold, Bernhard
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
FILE REFERENCE: HOOO1.NP0002
                                                                                                                                    NUMBER OF SEQ ID NOS: 39
                                                                                                                      SOFTWARE: PatentIn
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ORGANISM: Homo sapien
                                                                                     LENGTH: 235
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Pred. No. 1.2e-72;
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US-10-153-382-15
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                                                                GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
                                                                                                                                  Sequence 11, Application US/10153382 Publication No. US20030086930A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 15
LENGTH: 234
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/233042
PRIOR APPLICATION NUMBER: 60/233042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
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                               CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042 PRIOR FILING DATE: 2001-05-23
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Pred. No. 2.3e-64;
6; Mismatches 15
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7; Mismatches 12;
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SEQ ID NO 34
LENGTH: 236
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Patent No. US20020102658A1
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Best Local Similarity
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 11
LENGTH: 233
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Best Local
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR APPLICATION NUMBER: JP 2000-147116
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLOWAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM.
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
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TYPE: PRT
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                                                          121
                                                                         119 GQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN 178
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                                                                                                                            61 PGQAPGLLIYGASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQFGSSPMCSF
                                                                                                                                             60 PGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPW-TF
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SQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
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                                                      GQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGN
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90.3%;
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US-09-453-234-82
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                                                                         APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
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US-09-859-053-38
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                                      SEQ ID NO 82
LENGTH: 224
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APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. Us20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CUGRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-9508
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR APPLICATION NUMBER: JP 2001-99508
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PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 2e-62;
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VAIKITS, JOE

APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US.09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US.60/157,415
PRIOR TILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SEQ ID NO 88
LENGTH: 224
TYPE: PRT
RESULT 10
US-09-453-234-90
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                                                                                                                                                                                                                                                                                          LENGTH: 224
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: M2-34L
US-09-453-234-88
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US-09-453-234-88
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Best Local Similarity
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                                                                                                        SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 200
                                                                                                                                                                                        EIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRLLIYDTSNRATGIPA 80
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                                                                                             SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT
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95.88;
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95.8%;
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Pred. No. 7.5e-62;
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APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 90
LENGTH: 224
TYPE: PRT
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US-09-453-234-36
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; OTHER INFORMATION: M2-35L
US-09-453-234-90
                                                                                                                                                                                                                               APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
CURRENT FILING DATE: 1999-12-01
                                                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                   Query Match
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Best Local
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Best Local Similarity Matches 204; Conserv
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                                                                                         LENGTH: 224
TYPE: PRT
ORGANISM: Homo:
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/157,415 PRIOR FILING DATE: 1999-10-02 NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Buechler, Joe APPLICANT: Valkirs, Gun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Buechler, APPLICANT: Valkirs,
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Biosite Diagnostics, Inc.
 Conservative
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95.8%;
                  86.2%;
95.8%;
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Pred. No. 7.5e-62;
                  Score 1054; DB 11; Pred. No. 1.2e-61;
 Mismatches
1.2e-61;
7;
                                   Length 224;
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APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 84
                                                  US-09-453-234-46
Sequence 46, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
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Best Local :
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OTHER INFORMATION: M2-32L
-09-453-234-84
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APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
     APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
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                                                                                                                                                                                                                                                                                                                                                                                                                                          94.8%;
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Pred. No. 4.5e-61;
3; Mismatches 8;
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                                                                                                                                                                  Adkahara, Hideyuki

AANT: Tamaki, Ikuko

APPLICANT: Takahashi, Tohru

TITLE OF INVENTION: Anti-Fas Antibodies

FILE REFERENCE: 980126CIP/HG

CURRENT FILING DATE: 2002-08-09

PRIOR APPLICATION NUMBER: US/10/216,484

CURRENT FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: US/09/499,662

PRIOR APPLICATION NUMBER: US/09/499,662

PRIOR APPLICATION NUMBER: US 09/053,583

PRIOR FILING DATE: 1908-04-01

NUMBER OF SEO ID NOS: 165

CRGANTON
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORWATION: M1-10L
US-09-453-234-46
                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Designed light ; OTHER INFORMATION: chain of humanized anti-Fas ant.:body US-10-216-484-107
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US-10-216-484-107
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CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107, A Publication No.
                                                   Matches
                                                                  Best
                                                                              Query Match
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
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APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                  Local Sin hes 201;
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Similarity 84.5%; Pred. No. 7.1e-60;
01; Conservative 11; Mismatches 22;
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MEAPAQLLFLLLMLPDTTGEIVLTQSPATLSLSPGERAT).ACRASQT----ASRYLAWY
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Biosite Diagnostics, Inc.
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93.9%;
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Pred. No. 6.1e-61;
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GENERAL INFORMATION:

APPLICANT: TSU11, Takashi

APPLICANT: TSU14, Takashi

APPLICANT: HOT1, NO. US20020102658Aluaki

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: HHARMACEUTICAL USE THEREOF

FILE REFERENCE: 06501-079001

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT ETILING DATE: 2001-05-16

PRIOR APPLICATION NUMBER: JP 2001-99508

PRIOR APPLICATION NUMBER: JP 2000-147116

PRIOR APPLICATION ONUMBER: JP 2000-147116

PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 43

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 236
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US-09-859-053-30
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Search completed: September 12, Job time: 16.2034 secs
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Patent No. US20020102658A1
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Listing first 45 summaries
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Perfect score:
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1: /cgn2_6/ptodata/1
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-837-058-11
US-09-315-926A-79
US-09-315-926A-79
US-09-315-926A-79
US-09-171-945-97
US-09-485-737B-69
US-09-485-737B-69
US-09-485-737B-612
US-09-740-002-26
US-08-157-101A-5
US-09-485-737B-612
US-09-485-737B-62
US-09-740-002-26
US-08-740-002-26
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US-09-049-672A-6
                                                                                        TYPE:
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Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 6, Appli	∵		Sequence 2, Appli	Sequence 2, Appli	Sequence 40, Appl	Sequence 11, Appl				Sequence 39, Appl	Sequence 8, Appli	Sequence 25, Appl	•

ALIGNMENTS

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Sequence 6, Applia Patent No. 613594 GENERAL INFORMAT
                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for WI
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O
FILING DATE: HEREWITH
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER:
FILING DATE:
STRANDEDNESS: s
TOPOLOGY: linea
IMMEDIATE SOURCE:
LIBRARY: COLSUC
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                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,;
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650-845-4166
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                                                                                         234 amino acids
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Yue, Henry
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US-09-049-672A-6
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LENGTH: 234
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Best Local Similarity 85.9
Matches 201; Conservative
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APPLICANT: MORROW, PHILLIP
APPLICANT: MORROW, PHILLIP
ITTLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR APPLICATION NUMBER: 09/355,697
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR PILING DATE: 1999-06-18
PRIOR FILING DATE: 1995-06-07
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SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                         GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
                                                                                                                                                                                                                               GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                                            ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                                                                                                                                                   GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
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 Application US/09301593A
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80.8%; Pred. No. 1e-
tive 16; Mismatches
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LENGTH: 240
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6455677
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APPLICANT: Garin-Chesa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       ADDRESSEE: The Scripps Research Institute, Office ADDRESSEE: Patent Counsel STREET: 10666 NO. 5652138th Torrey Pines Road, Sui STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA
                                                                                                                                            COUNTRY: USA
ZIP: 92037
FILING DATE:
                  APPLICATION NUMBER:
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 18-JUL-1994
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                  US/08/276,852
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Pred. No. 8
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                                                     Version
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US-08-899-575-153
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Best Local Similarity 82.1
Matches 193; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 153,
                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION MADAER: US/08/899,575
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                             APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: 'Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
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                                                                                                                                                                     ADJAKESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
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REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SC
                                                                                                                                            COUNTRY: U. ZIP: 92037
CLASSIFICATION:
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                                                                                                                                                             USA
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82.1%; Pred. No. 1.6e-72;
tive 14; Mismatches 27;
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; MOLECULE TYPE: protein US-08-899-575-153
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US-08-899-575-153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Burton, Dennis K
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
                                                              CURRENT APPLICATION DATA
                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                     ADDRESSEE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220. STREET: Mail Drop TPC8
                                  APPLICATION NUMBER: US/08/899,575 FILING DATE: 24-JUL-1997
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/276,852 FILING DATE: 18-JUL-1994
                  CLASSIFICATION
                                                                                     SOFTWARE:
                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                         ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
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                                                                                       PatentIn Release #1.0, Version
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82.1%; Pred. No. 1.6e-72;
Live 14; Mismatches 27;
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RESULT 7
PCT-US95-08743-153
Sequence 153, Application PC/TUS9508743; GENERAL INFORMATION:
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                                                          ; MOLECULE TYPE: PCT-US95-08743-153
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                Best
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                              Query Match
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Best Local Similarity
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APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                       APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
  Local Similarity
nes 193; Conserv
                                                                                     TOPOLOGY:
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                                                                                                              LENGTH:
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    Conservative
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18-JUL-1994
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              80.0%; Score 978.5;
82.1%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.0%; Score 978.5; DB 1;
82.1%; Pred. No. 1.6e-72;
82.1%; Mismatches 27;
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 Mismatches
                1.6e-72;
                           DB 5;
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 27;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-812-586-16
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US-08-812-586-16
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                                                                                                     Matches
                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                     TELEFAX: (212) 391-0525 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Martin Da
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1185 AVE
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                                                    TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/812,586 FILING DATE: 07-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                   Local
                                                                                                                                                                                                                                                     LENGTH:
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61 GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
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                                                                  1 MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                 h 80.0%;
Similarity 84.1%;
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                                                                                                                                                                                                                                    amino acids
                                  MGVPTQVLGLLLLWLTDARCEIVLTQSPGTLSLSPGERATFSCRSSHSIRSRRVAWYQHK
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1185 Avenue of the Americas
                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARTIN DAVID TILSON
VENTION: PURIFIED AND RECOMBINANT ANTIGENIC
VENTION: PURIFIED AND RECOMBINANT ANTIGENIC
VENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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                                                                                                                   Score 978; DB 3; Pred. No. 1.7e-72;
                                                                                                     Mismatches
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                                                                                                     29;
                                                                                                                                  Length 235;
                                                                                                     Indels
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                                                                                                 Gaps
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GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180

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; ORGANISM: Homo sapiens
US-09-535-832A-17
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US-09-535-832A-17
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APPLICANT: Tilson, Martin David
TITLE OF INVENTION: With Abdominal Aortic Aneurysm (AAA) Disease, and
TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 17, Application US/09535832A
Patent No. 6537769
                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                      Sequence 56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT: BURKLY
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CURRENT APPLICATION NUMBER: US/09/535,832A
CURRENT FILING DATE: 2000-03-28
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                                                                                                                              TITLE OF INVENTION: ANTI-CD4 ANTIBODY FITTLE OF INVENTION: PROPHYLAXIS AND TRE NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD. STREET: 10 SOUTH WACKER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 235
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
OPERATING SYSTEM: PC-DOS
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                                                                                                                     CITY: CHICAGO
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                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           183
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                                                                      60606
                                                                                                                                                                                                                                                                                                                                     6, Application US/07916098A 5871732
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                                                                                                      ILLINOIS
                                                                                                                                                                                                                                    ROSA, MARGARET D. ROSA, JOSEPH J.
                                                                                                                                                                                                                                                                   CHISHOLM, PATRIC THOMAS, DAVID W.
                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                       BURKLY, LINDA C
      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80.0%;
                                                                                                                                                                                                   ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN PROPHYLAXIS AND TREATMENT OF AIDS, A
                                                                                                                                                                                                                                                                                      PATRICIA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 978; DB 4; Pred. No. 1.7e-72; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 235;
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                                                                                                                                                                                                       HIV INFECTION
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US-08-480-753-6
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                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08480753 Patent No. 5830675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendy A. Whiteford, E.
STREET: 444 South Flower Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
TITLE OF INVENTION: PERINUCLEAR ANTI-REUTROPHIL CYTOPLASMIC ANTIBODY OF
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITIS,
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                   APPLICANT: Targan M.D., Stephan R APPLICANT: Vidrich Ph.D., Alda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (314, 5317)
TELEX: 910/221-5317
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/
FILING DATE: July 24, 1992
                                                                                                                   CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE:
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REFERENCE/DOCKET · NUMBER: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: No CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
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190; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PWTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASV\CLLNNFYPREAKVQWKVDNAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MRVPAQLLGLLLLWLPGARGDIVMTQSPDSLAVSLGERATINCKSSGSLLYSTNQKNYLA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEAPAQLLFLLLLMLPDTTGEIVLTQSPATLSLSPGERAFLACRA-----SQTASRYLA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 amino acids
                                                                                                      USA
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(312) 715-1234
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DN: 424
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79.28;
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Whiteford, Esq.
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; Pred. No. 7.3e-72;
18; Mismatches 25;
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     Version #1,25
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CURRENT APPLICATION DATA:

07-JUN-1995

US/08/480,753

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SEQUENCE CHARACTERISTICS:
TRUNGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 603300
Patent No. 603300
Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local Similarity
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                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof,
TITLE OF INVENTION: Microbial UC pANCA antigens
                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 11-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 36,964
REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
TELEPHONE.
                             FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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   REGISTRATION NUMBER:
                                                                                           CLASSIFICATION:
                                                                                                           FILING DATE:
                                                                                                                         APPLICATION NUMBER:
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NO. 6033864
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                 Campbell,
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Cathryn A.
BER: 31,815
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88.7%;
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Pred. No. 2.8
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RESULT 13
US-08-837-058-11
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INFORMATION FOR SEQ ID NO:
                                   TELEFAX: (619) 535-89 INFORMATION FOR SEQ ID NO:
                                                                                                   APPLICATION NUMBER: US/08/8:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-
                                                                                                                                                                                                                         COMPUTER: IBM PC. compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
. SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      ZIP: ZIP: ZIP: COMPUTER READABLE FORM:
MENTUM TYPE: Floppy disk
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APPLICANT:
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Histone H1
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LENGTH: 214 amino acid
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                                                     535-8949
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88.78;
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Pred. No. 2.
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                                                                                                                                                                                                                                             Version
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TOPOLOGY: 11;
HOLECULE TYPE:
US-09-417-264-11
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US-09-417-264-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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 Matches
            Query Match
Best Local Similarity
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,88
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 9-PM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10535-0001
                                                                                                                                                      TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtyr
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4370 La Jo. CITY: San Diego STATE: California COUNTRY: USA
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4370 La Jolla Village Drive, Suite 700
 Conservative
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88.7%;
              78.7%;
88.7%;
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              Score 962.5; DB Pred. No. 2.8e-71
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APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A (
FILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 99201593.3
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 236
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; 'LOCATION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79
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APPLICANT: Es van, Helmuth
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                                                                                                                                                                                                                        Matches 194;
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Best Local (
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OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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Similarity 82.9%;
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Pred. No. 3.2
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Submitted (JUN-2002) to the EMBL/GenBank/DDBJ da:abases.
EMBL; BC030813; AAH30813.1; -.
R InterPro; IPR0077110; Ig-1ike.
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Q8NEK1;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
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                                                                           Chordata; Craniata; Vertebrala; Euteleostomi; Primates; Catarrhini; Hominidae; Homo
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Hypothetical protein.
Homo sapiens (Human).
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SMART; SM00407; IGC1; 1.

SMART; SM00406; IGC; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; 1.
    Eukaryota;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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SEQUENCE 23
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Pred. No. 9.1
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Mismatches
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    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239;
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                                                             Query Match
Best Local S
Matches 135
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Best Local S
Matches 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q99M37 PRELIMINARY; PR
Q99M37; O1-JUN-2001 (TrEMBLrel. 17, Crea
01-JUN-2001 (TrEMBLrel. 17, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMB Submitted (FEB-2002) to the EMB EMBL; BC022362; AAH22362.1; -.
InterPro; IPR007110; Ig-1ike. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 2.
Pfam; PF00047; Ig; 2.
PART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26234 MW;
                                                                                                                                                                                     HSSP; P01679; 2FBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (JAN-2001) to the
EMBL; BC002035; AAH02035.1;
HSSP; P01679; 2FBJ
                                                                                                                                                Hypothetical SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Lung
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                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                al protéin.
238 AA; 2
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                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A.
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                                                                                                                                                  26344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates; Catarrhini; Hominidae; Homo.
                                                                                   59.6%;
56.5%;
                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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                                                             Score 729; DB 11;
Pred. No. 1.5e-61;
4; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 956.5; DB 4;
Pred. No. 2.7e-83;
8; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FACEDC3A3B03871D CRC64;
                                                                                                                                                FB2B06A0B801330A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                      DB 11;
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                                                                                                      Length
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                                                                                                         238;
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RESULT Q8VC16
Q8VC16
Q0 Q8
AC Q8
AC Q8
AC Q10
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Best Local :
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01-MAR-2003 (TYEMBLrel. 20, Last sequence update)
01-MAR-2003 (TYEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse).
Eukaryota: Metanno.
                                                         Q8VCI6 PRELIMINARY; PRT; 238 AA.
Q8VCI6;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
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Q8VCPO;
01-MAR-2002
     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                            Mus musculus (Mouse).
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 234 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2001) to the EMBL; BC019474; AAH19474.1; InterPro; IPR003006; Ig_MHC. InterPro; IPR003599; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Submitted (DEC
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                             GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GKSPQLLYNAKTLADGVPSRFSGSRSGTQFSLKINSLQPEDFGSXYCQHHSGIPFTFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEAPAQLLFLLLHMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25702 MW;
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Pred. No. 4.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL/GenBank/DDBJ databases
  Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102551C58AC2FA9F CRC64;
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  Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
; Murinae; Mus
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δÃ
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Best Local
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Submitted (APR-2002) to the EMI
Submitted (APR-2002) to the EMI
EMBL; BC027418; AAH27418:1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8R062 PRELIMINARY; PRT; 234 AA. 08R062; O1-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                  PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases EMBL; BC019760; AAH19760.1; -.
                                                                                                                                                                                                                                                      Hypothetical protein. SEQUENCE 234 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 WTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVC:LLNNFYPREAKVQWKVDNALQ 175
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34; Conservative
                                                                                                                                                                            Similarity
  GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSIS5LEPEDFAVYYCQQRFNWPWTFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPG::RATLACRASQTASRYLAWYQQKP
                                                    MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLG')RVTISCSASQGISNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYT; EATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVV(!FLNNFYPKDINVKWKIDGSER
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                        25857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.9%;
56.1%;
                                                                                                                                                                          58.0%; Score 709; DB 1:; 58.1%; Pred. No. 1.2e-5!);
                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 720; DB 11;
Pred. No. 1.1e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                                                                                                                                                                                                      4EB08C81426AEAF1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35EC08E3DE5414AD (!RC64;
                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             upćate)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Muridae;
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; Murinae; Mus
                                                                                                                                                  0;
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Best Local S
Matches 132
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EMBL; BC031498; AAH31498.1; .

InterPro; IPR003198; ADH_short.

InterPro; IPR003599; Ig.

InterPro; IPR003597; Ig.cl.

InterPro; IPR003596; Ig_MHC.

InterPro; IPR003066; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 2.

SMART; SM00409; IG; 2.

SMART; SM00406; IGv; 1.
                Q91WF8;
01-DEC-2001
01-DEC-2001
01-MAR-2003
      Hypothetical
                                                                                 Q91WF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE: PS00061; ADH_SHORT: PROSITE: PS00290; IG_MHC; 1. Hypothetical protein. SEQUENCE 239 AA; 26366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammaila; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8K0F8;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                        LLQRPGQSPKRLISLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP
                                                                                                                                                                                                                                                                                                    GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l protein.
239 AA; 26366 MW; D7BE84398AA341F0 CRC64;
 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
L 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        57.48;
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                                                                                                                                                                                                                                                                                                                                                                                                             43;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 702.5;
Pred. No. 5.2
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Sciurognathi;
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                               59;
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Best Local S
Matches 132
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Best Local Sin
Matches 136;
                                                                                                         Submitted (JAN-2002) to the EMEL; BC021781; AAH21781.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 239 AA; 26303 MW;
                                                                                                                                                                                                                                                                                                          Q8VC55 PRELIMINARY; PR
Q8VC55;
01-MAR-2002 (TrEMBLrel. 20, Crea
01-MAR-2002 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Eukaryota; Wetazoa; Chordata; Cr.
Mammalia; Eutheria; Rodentia; Sc.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 234 AA; 25929 MW; BODOBOE6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001865; R Pfam; PF00047; ig; 2. SMART; SM00406; IGv; 1
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[1]
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
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                                               Local Similarity
mes 132; Conserv
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BC015292; AAH15292.1; -
PFO; IPR003006; Ig_MHC.
PFO; IPR003396; Ig_v.
PFO; IPR001865; Ribosomal_S2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQT--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMSSAQFLGLLLLCFQGTRCDTQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Rođentia;
                                                                                                            26303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57.3%;
58.1%;
                                               57.3%; Score 700.5; DB 11; 55.2%; Pred. No. 8.1e-59; tive 43; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34;
                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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Pred. No. 7.1e-59;
4; Mismatches 64
                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                            C16119CACA25C337 CRC64;
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ data Submitted (SEP-2001) to the EMBL/GenBank/DDBJ data Submitted (SEP-2001); Ig-like.

RefinerPro; IPR007110; Ig-like.
RefinerPro; IPR003596; Ig_MHC.
RefinerPro; IPR003596; Ig_V.
RefinerPro0047; ig; 2.
RefinerPro0047; ig; 2.
RefinerPro0047; ig; 1.
RefinerPro0047; ig; 2.
RefinerPro0
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Best Local :
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 25.8 kDa protein (Fragment).
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mammalia; Eutheria; Rodentia; Sciurognathi; Murid
Q91W12;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence up
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation
Unknown (Protein for MGC:6582).
                                                                                                                                                        Q91W12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRLLIYD 70
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                                                                                                                                                        PRELIMINARY;
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Pred. No. 7.9e-58;
5; Mismatches 59;
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                                                                                                                                                        PRT;
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InterPro; IPR0077110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_WC.
InterPro; IPR003956; Ig_V.
Pfam; PF00047; Ig; 2.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS01835; IG_LIKE; 2.
PROSITE; PS01990; IG_MHC; 1.
SEQUENCE 235 AA; 26021 MW; 5FC73BDEBD5E8FEF
                                                                                                                                              Pfam; PF00047; 19; 2;
SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
PROSITE; PS00290; IG_M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RIA5 PRELIMINARY; PRT; 214 AA. Q9RIA5; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence up 01-MAR-2003 (TrEMBLrel. 23, Last annotation Kappa light chain of Mab7 (Fragment). Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                            Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rantibody (Mab 7, its light and heavy chains) and construsingle chain antibody (scFV)."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF152371; AAD40242.1; -...
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                        NON_TER
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Submitted (APR-2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                     PS50835; IG_LIKE PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQK;GQAPRLLIYDTSNRATGIP 79
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                                                               AA;
                                                                                                                                                                              IG_LIKE;
                                                                                                                                                                                                                                             <u>ب</u>
                                                               23922 MW;
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   55.3%;
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   Score 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lah A.K.M., Misra S.;
anti-white pine blister rust monoclonal
heavy chains) and construction of a
                                                               52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5FC73BDEBD5E8FEF CRC64;
   DВ
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RESULT 15
Q8TBC9
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AC Q8TBC
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Matches 126
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Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (APR-2002) to the EM
EMBL; BC028540; AAH88540.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IG; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25702 MW;
 Q8TBC9;
Q8TBC9;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Mammary gland;
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                                                                                                                                                                                                                                                                                                                                                                                     AQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAP
                                                                                                                                                                                                                                  ELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT
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 (TrEMBLrel.
                                                           PRELIMINARY;
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                   Created)
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 Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 655; DB 11;
Pred. No. 1.8e-54;
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7; Mismatches 54;
                                                           PRT;
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Murinae; Mus
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Best Local
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022823 AAH22823.1;
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                          Hypothetical protein. SEQUENCE 233 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                              rissue-B-cell;
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completed: ne : 42.6525
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                                                                                                                                                                                                                                           Similarity 43.1
00; Conservative
                                                                                                                                                          LIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQ--QRFNWPWTFGQGTKV 124
                                             TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTEC
                                                           VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                          LLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRL
                                                                                              TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG--VET
                                                                                                                                            VIYKDNERPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYWVFGGGTKL
                                                                                                                                                                                            LLLPLLTLCTGSEASYELTQ-PPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVL
           September
                                                                                                                                                                                                                                                     37.5%;
                                                                                                                                                                                                                                                                                           24867 MW;
           12,
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                                                                                                                                                                                                                                          41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last annotation
                                                                                                                                                                                                                                                     Score 458.5; DB 4
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           367411BFD6F4DF92 CRC64;
            13:03:29
                                                                                                                                                                                                                                                                DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                           82; Indels
                                                                                                                                                                                                                                           9;
                                                                      234
                                                232
                                                                                                                                                                                                                                          Gaps
                                                                                                                      182
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Perfect score:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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KV3H_HUMAN
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homo sapien
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KV3I_HUMAN STANDARD; PRT; 115 AA.

ID KV3I_HUMAN STANDARD; PRT; 115 AA.

AC p04433;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-UL-1999 (Rel. 38, Last annotation update)
DT 15-UL-1999 (Rel. 38, Last annotation update)
DE 19 kappa chain V-III region VG precursor (Fragment).
OS HOMO sapiens (Human).
OC ELLKATYOCIA: Metazoa; Chordata; Craniata; Vertebrati; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RR MEDLINE=65087932; PubMed=6440122;
RA PECH M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are ..nterdigitated within the VK locus.";
RL Nucleic Acids Res. 12:9229-9336(1984).
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ALIGNMENTS

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Query Match 46.4%; Score 568; DB 1; Best Local Similarity 93.9%; Pred. No. 3.1e-41; Matches 108; Conservative 3; Mismatches 4	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinformat the European Bioinformatics Institute. The swiss Institute of Bioinform the European Bioinformatics Institute. The statement is not removed and this statement is not removed entities requires a license agreement (Secon Send an email to license@isb-sib.ch). EMBL; X01668; -, NOT_ANNOTATED_CDS. PIR; A01900; K3HUVG. PIR; A01900; K3HUVG. INTL. GO; GO:0003576; C:extracellular; NAS. GO; GO:0003576; C:extracellular; NAS. GO; GO:0005955; P:immune response; NAS. InterPro; IPR007110; Ig-like. InterPro; IPR003106; Ig_MHC. InterPro; IPR003596; Ig_w. PFAMEWORA; 19; 1. SMART; SM00406; IGV; 1. PROSITE; PS50835; IG_LIKE; 1. Immunoglobulin V region; Signal. SIGNAL CHAIN 21 >115 DOMAIN 70 76 COMPLEMENTAR. DOMAIN 77 108 DOMAIN 109 115 SEQUENCE 115 AA; 12575 MW; 2DE47CD3A.	RL Nucleic Acids Res. 12:9229-9236(1984).
;	produced through a collaboration atics and the EMBL outstation here are no restrictions on its as its content is in no way discontent is in no way by and for commercial http://www.isb-sib.ch/announce/ y; NAS. y; NAS. IN V-III REGION VG. ITY-DETERMINING-1. ITY-DETERMINING-3. Z.	

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RESULT 2

KV3H_HUMAN
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGV;
PROSITE; PS50835; IG
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Mammalia; Eutheria; Primates;
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GO:0003823; F:antigen binding activity;
GO:0006955; P:immune response; NAS.
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GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNW-PWTFG
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83.7%;
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region CLL precursor (Rheumatoid factor).
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3; Mismatches
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Pred. No. 8.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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J. EXP. Med. 167:840-852(1988).
-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light.chain variable region expressed in chronic lymphocytic leukemia with little or no mutation. Implications for etiology and immunotherapy.";
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SMART; SM00406; IGv; 1.
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
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HSSP; P80362; 1WTL.
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01-NOV-1990 (Rel. 16, Last sequence update
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Ig kappa chain V-III region HIC precursor.
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P18136;
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Pred. No. 1e-40;
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FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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"Autoantibody-associated kappa light chain variable region expressed in chronic lymphocytic leukemia with little or no mutation. Implications for etiology and immunotherapy.";
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Eukaryota; Metazoa; Chordata; Craniata
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SMART; SM00406; IGv;
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-!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN
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  kappa chain
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NA
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Pred. No. 5.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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JK1 SEGMENT.
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Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from ahdominal subcutaneous fat biopsy: kappa IV immunoglobulin light c Biochem. Biophys. Res. Commun. 245:713-716(1998)
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV |3) ALLOT 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE IIV (1,2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suter I., Barnikol H.U., Watanabe S., Hilschmann N.;
"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones proteri). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
hoppe-Seyler's Z. Physiol. Chem. 353:189-208(197:).
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(In) Franck F., Shugar D. (eds
Gamma globulins: structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=81042304; PubMed=6775818;
Hieter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr.,
"Cloned human and mouse kappa immunoglobulin con:tant
genes conserve homology in functional segments."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebratı; Mammalia; Eutheria; Primates; Catarrhini; Hominidia;
                                                                             PubMed=9588180;
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                                                                                                                                                                                                                         Biol.
                                                                                                                                                                                                                      amino acid sequence of a kappa type Bence-Jones protein. lete sequence and the location of the disulfide bridges."; iol. Chem. 244:3550-3560(1969).
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man gamma G-immunoglobulin.
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InterPro; IPR00397; Ig_cl.
InterPro; IPR003906; Ig_MHC.
Pfam; PF00047; Ig; 1.
SMART; SM00407; IGCl; 1.
PROSITE; PS50825; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PDB; 1D5B; 09-FEB-00.
PDB; 1D5I; 09-FEB-00.
PDB; 1D5V; 04-OCT-00.
PDB; 1HEZ; 10-AUG-01.
PDB; 1HKL; 12-MAR-97.
PDB; 117Z; 08-AUG-01.
PDB; 117X; 08-AUG-01.
PDB; 1HKM; 15-MAY-97.
Genew; HGNC: 5716; IGKC.
MIM; 147200;
                                                                                                      01-JAN-1988 (Rel. 06, Create
01-JAN-1988 (Rel. 06, Last s
15-JUL-1999 (Rel. 38, Last a
19 kappa chain V-III region
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                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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             SEQUENCE FROM N.A. MEDLINE-86041852; Klobeck H.G., Mein
                                                           NCBI_TaxID=9606;
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Last annotation (
region IARC/BL41)
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V -> L (IN INV(1,2) MARKER)
/FTId=VAR_003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
W; 51984D1FDD372CE8 CRC64;
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Pred. No. 1.4e-39;
                                                                     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region; S:
                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                         HUMAN
  Nucleic
            Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups
within the VK locus.";
                                               SEQUENCE FROM N.A. MEDLINE-85087932;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0003823; P:immune response; NAS.
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HSSP; P01607; 1REI.
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                                                                                 NCBI_TaxID=9606;
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
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BY SIMILARITY.
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Pred.
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 PIR; A01892; K3HUSI.
HSSP; P80362; lWTL.
GO; GO:0005576; C:ext
GO; GO:0003823; F:ant
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SEQUENCE
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Andrews D.W., Capra J.D.;
*Amino acid sequence of the variable
*Amino acid sequence of the human Iq
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat.
Ig kappa chain V-III region SIE.
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                                                                              Biochemistry 20:5816-5822(1981)
                                                                                                                                                                               NCBI_TaxID=9606;
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                                                   MISCELLANEOUS: THIS GLOBULIN ACTIVITY.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Ig kappa chain V-III region Ti.
Homo sapiens (Human).
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PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
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Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972)
-i- MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS
-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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DISULFID 23 89 BY SIMILARITY.
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HSSP; P80362; 1WTL.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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InterPro; IPR003596; Ig_v.
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SMART; SM00406; IGv; 1.
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Immunoglobulin V region.
DISULFID 23 89
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Homo sapiens (Human).
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Homo sapiens (Human).
Homo sapiens (Human).
Horizota; Metazoa; Chordata; Metazoa; Chordata; Metazoa; Chordata; Metazoa; Meta
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P01624;
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21-JUL-1986 (Rel. 01, Last sequence update)
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Ig kappa chain V-III region WOL.
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Klapper D.G., Capra J.D.;
"The amino acid sequence of the variable regions of t from two idiotypically cross reactive IgM anti-gamma Ann. Immunol. (Paris) 127C:261-271(1976).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IC GLOBULIN ACTIVITY.
PIR; A01897; K3HUPM.
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16-0CT-2001 (Rel. 40, Last annotation update)
1g kappa chain V-III region POM.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
       Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains
"Amino acid sequence of the variable regions of light chains
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                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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KV3G_HUMAN
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Best Local S
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Best Local
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003396; Ig_v.
Pfam; PF00047; Ig; 1
SMART; SM00406; IGv; 1
PR0SITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region.
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HSSP, P80362; IWTL.
GO; GO:0005576; C:extracellular; NAS:
GO; GO:0003823; F:antigen binding act
GO; GO:0006955; P:immune response; NA
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-86230578; PubMed-3086710;
Newkirk M., Chen P.P., Carson D.A., Posnett D.,
"Amino acid sequence of a light chain variable
rheumatoid factor of the Wa idiotypic group, in
reactivity with antipeptide antibodies.";
mol. Immunol. 23:239-244(1986).
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20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Cast annotation date)
15-Kappa chain V-III region GOL (Rheumatoid fi
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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-!- MISCELLANEOUS: THIS CHAIN W
                                                                                        SEQUENCE
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109 AA;
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                                                                                        11830 MW;
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80.7%;
  Score 441.5;
Pred. No. 1.3e
8; Mismatches
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EIVLTQSPATLSLSPGERATLACRASQTASR-YLAWYQQKPGQAPRLLIYDTSNRATGIP

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RESULT 13

KV4C_HUMAN
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GO; GO:0003823; F:antigen binding activ
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_W.
PR0STTE; PS0047; Ig; 1.
SMART; SM00406; IGV; 1.
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                                                                                                                                                                                                                                                                                                   DOMAIN
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01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-IV region B17 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa cDNA probe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=86041854; PubMed=2997713;
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Mammalia; Eutheria; Primates; Catarrhini;
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17; Mismatches
                                                                                  Score 432; DB 1;
Pred. No. 1.1e-29;
7; Mismatches 28;
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COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                               FRAMEWORK - 2.
COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                         IG KAPPA CHAIN V-IV REGION B17 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
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RESULT 14

KV3A_HMAN

ID KV3A,H

ID KV3A,H

P01619

AC P01619

DT 21-JUL

DT 15-JUL

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CC Eukary

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Best Local
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                                                                                                                                                                                                                            P06310;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig kappa chain V-II region RPMI 6410 precursor.
Homo sapiens (Human).
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat.
Ig kappa chain V-III region B6.
Homo sapiens (Human).
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P01619;
                                 SEQUENCE FROM N.A.
MEDLINE=86041852; PubMed=2997711;
Klobeck H.G., Meindl A., Combriato G., S
"Human immunoglobulin kappa light chain
                                                                                                                                                          Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Nucleic
                                                                                                                                                                                                                                                                                                                                                                          KV2F_HUMAN
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DISULFID 23 89 BY SIMILARITY.
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InterPro; IPR007110;
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108
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13:6499-6513(1985)
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75.0%;
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Pred. No. 1.9e-29;
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                                         n A., Zachau H.G.;
of subgroups II and
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Best Local S
Matches 78
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SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

IMMUNOGIOBULÍN V region; Signal.

SIGNAL 1 20
CHAIN 21 13 FRAME
DOMAIN 44 59 COMPL
DOMAIN 60 74 FRAME
DOMAIN 75 81 COMPL
DOMAIN 82 113 FRAME
DOMAIN 82 113 FRAME
DOMAIN 114 122 COMPL
DOMAIN 123 133 FRAME
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DOMAIN 126 133 FRAME
DOMAIN 127 FRAME
DOMAIN 128 133 FRAME
DOMAIN 129 130 FRAME
DOMAIN 120 131 BY SI
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NON_TER 133 AA; 14707 MW; 513
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PIR; A01890; K2HURP.
HSSP; P80362; IMTL.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0077110; Ig-1ike.
InterPro; IPR00306; Ig-MHC.
InterPro; IPR00396; Ig-W.
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116 WTFGQGTKVEFKR 128
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|121 WTFGQGTKVEIKR 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         35.0%; Score 427.5; DB 1
58.6%; Pred. No. 2.5e-29;
Live 24; Mismatches 26
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
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COMPLEMENTARITY-DETERMINING-2.
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Search completed: September 12, 2003, 13:01:16 Job time: 10.9153 secs

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Result
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Maximum Match 1008
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Perfect score:
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length: 2000000000
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Gapop 10.0 ,
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    GenCore version (c) 1993 - 2003
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                           RESULT 2
JE0244
JE0244
Ig kappa chain NIG2 precursor - human
C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C; Accession: JE0244
R; Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998
A; Description: A new subgroup of k type light chains (VkV) identified in cases of A A; Reference number: JE0243
A; Molecule type: protein
A; Residues: 1-215 <ALI>
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F;16-90/Domain: immunoglobulin homology
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	2 \$40328	131	44.5	544.5	45
Ig kappa chain pre	2 S11697	115	44.6	545	44
Ig kap	2 S23628	111	44.6	545	ω
Ig lar	2 A49633	238	44.7	546.5	2
Ig kap	2 S20636	128	44.8	547.5	ت
Ig kap	1 K3HU	106	44.8	548	ö
anti-s	2 S49532	129	45.2	552.5	39
Ig kap	1 КЗНИНА	129	45.3	553.5	8
Ig kap	2 S40363	129	46.0	562.5	37
Ig kap	1 K3HUHI	129	46.0	562.5	8
Ig kap	2 A20969	229	46.1	563.5	35
Ig ka _l	2 S40343	128	46.2	565	4
Ig kaj	1 K3HUVG	115	46.4	568	చ
Ig ka _l	2 S40345	128	46.5	569	2
Ig kap	2 S29593	197	47.1	575.5	Ξ
Ig kap	2 S29627	129	47.6	582	ö

ALIGNMENTS

RESULT 1 JE0242 Ig kappa chain NIG26 precursor - human C; Species: Homo sapiens (man) C; Date: 05-Dec-1998 #sequence_revision 05-Dec; Dacession: JE0242 R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Tak submitted to JIPID, November 1998 A; Description: Structure relationship of kay ****coference number: JE0241 A;Molecule type: protein A;Residues: 1-215 <ALI> C;Superfamily: immunoglobulin V region; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM> TLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 82.6%; 91.6%; Score 1010.5; DB 2; Pred. No. 1.1e-62; 4; Mismatches 13; 05-Dec-1998 kappatype Takeda, K.; 215 light chains with AL amyloidosis: #te::t_change 2 Kojima, M.; Takashi, I.; Shinoda homology Indels Length 215; 21-Jan-2000 1; Gaps 60

immunoglobulir, homology
<IMM>

ΑŁ

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RESULT 4
A23746
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C;Species: Homo sapiens (man)
C;Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 2
C;Accession: A23746
R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A;Title: The primary structure of the Fab fragment of protein KAU
A;Reference number: A23746; MUID:91131575; PMID:1993660
A;Accession: A23746
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3

JE0243

Ig kappa chain NIG93 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change

C;Accession: JE0243

R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.;

submitted to JIPID, November 1998

A;Description: A new subgroup of k type light chains (VkV) ident

A;Reference number: JE0243

A;Accession: JE0243

A;Accession: JE0243
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Matches 192
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                                                                                                                                                                                                                             TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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immunoglobulin homology
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89.3%;
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Pred. No. 7.6e-
7; Mismatches
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Pred. No. 5e-
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No. 7.6
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Ig kappa chain Am37 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-05-Dec-1998
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Talsubmitted to JIPID, November 1998
A;Description: Structure relationship of kappatype light chains with A;Reference number: JE0241
A;Reference number: JE0241
A;Reference number: JE0241
A;Rolecule type: protein
A;Residues: 1-216 <ALLI-
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-92/Domain: immunoglobulin homology <IMM>
Ig kappa chain precursor - rat (Species: Rattus norvegicus (Norway rat) C; Species: Rattus norvegicus (Norway rat) C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change C; Accession: S06084 R; Crowe, J.S.; Smith, M.A.; Cooper, H.J. Nucleic Acids Res. 17, 7992, 1989 A.; Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunog A; Reference number: S06084; MUID:90016888; PMID:2508067 A; Accession: S06084
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76.6%;
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89.78;
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6; Mismatches
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Pred. No. 1.6e-51;
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immunoglobulin kappa chain

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A; Molecule type: mRNA
A; Residues: 1-240 <CRO>
A; Residues: 1-240 <CRO>
A; Cross references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
A; Cross references: EMBL:X16129; NID:g56457; immunoglobulin homology
C; Seywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Molecule type: mRNA
A;Residues: 1-234 <DE1>
A;Residues: 1-234 <DE1>
A;Cross-references: EMBL:X13187; NID:g51784; PIDN:CAA31579.1; PID:g51785
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                           F;1-20/Domain: signal sequence #status predicted <SIG>F;21-234/Product: Ig kappa chain #status predicted <MAF;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A;Reference number: S01320; MUID:88329081; PMID:3138116
A;Accession: S01320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain precursor - mouse
C;Specites: Mus musculus (house mouse)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C;Accession: S01320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, Eur. J. Biochem. 176, 287-295, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               맑
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                                                                                                                                    PWTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WYQQKPGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRENW 114
                                                                                                                                                                                    GKSPQLLVYVATKLVDGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWDTPFTFGS
                                                                                                                                                                                                                    GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                                                                                                                                                                                      MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGESVTITCRASENIYSNLAWYQQKQ
                                                                                                                                                                                                                                                                                       MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYTFGAGTKLELKRADAAPTVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEAPAQLLFLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQT-----ASRYLA 54
                                              NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                GTKLEMKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MESQTQVLMSLLLWISGTCGDFVMTQSPSSLAVSAGETVTINCKSSQSLFYSGNQKNYLA
                                                                                  ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                          Score 727; DB 2;
Pred. No. 3.5e-43;
7; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 771; DB 2;
Pred. No. 3.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                              <MAT>
                                                                                                                                                                                                                                                                                                                                                         Length 234;
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A; Accession: S33161
A; Status: preliminary
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A; Residues: 1-234 <VAN>
                                                                                                                                                                                                                    Matches
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136; Conserv
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56.8%;
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A;Molecule type: mRNA
A;Residues: 1-230 <FOL>
A;Residues: 1-230 <FOL>
A;Cross-references: EMBL:X54110; NID:g297103; PIDN:CA#38046.1; PID:g1364221
C;Superfamily: immunoglobulin V region; immunoglobulir homology
C;Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig kappa chain - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (dcmestic sheep)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S33161
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A;Title: Construction and characterization of a recombinant murine monoclonal antibo A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Foley, R.C.; Beh, K.J. submitted to the EMBL Data Library, July 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X56394; NID:g51622; P;C;Superfamily: immunoglobulin V region; immunogC;Kupwords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
                                                                                                                         61 KLLIYYATRLHTDVPSRFSGSGSGTDYTLTISNLEANDTFTYYCLQYESTPLAFGGGTNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
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                                                                                                                                                   RLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFFVYYCQQRFNWPWTFGQGTKV
                                                                                                                                                                                                                                             QLLGLLLLMLLPGARCDIQVTQSPSSLSASLTERVSITCFTSQSVSNYLNWYQQKPGQAP
                                                                                                                                                                                                                                                                          QLLFLLLLW-LPDTTGEIVLTQSPATLSLSPGERATLACFASQTASRYLAWYQQKPGQAP
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EIKRSDAQPSVFLFKPSEEQLRTGTVSVVCLVNDFYPKDINVKVKVDGVTQNSNFQNSFT
                                                         EFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPRE#KVQWKVDNALQSGNSQESVT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCKASQDINSYLSWIQQKP
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                                                                                                                                                                                                                                                                                                                                                                57.5%; Score 703.5; DB 2
59.1%; Pred. No. 1.4e-41;
tive 35; Mismatches 58
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Pred. No. 1.7e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of sheep kappa light chain cDNA.
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RESULT 10
$38865

If kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: $38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
submitted to the EMBL Data Library and desired
**Peacription: Combination of a defined specificity and desired
                                                                                                                                                                                                                           A; Molecule type: mRNĀ
A; Residues: 1-225 < DUC>
A; Residues: 1-225 < DUC>
A; Cross-references: EMBL: X70424; NID: g406254; PIDN: CAA49869.1; I
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                         Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S37484
R;Ducancel, F.F.D.
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A; Residues: 1-219 <KTP>.
A; Residues: 1-219 <KTP>.
A; Cross-references: EMBL: 227396; NID: g416538; PIDN: CAA81787.1; PID: g416539
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: Combination
A; Reference number: S38864
A; Accession: S38865
A; Status: preliminary
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A; Status: preliminary
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                                                                                                                                                           Query Match
Best Local S
Matches 132
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Best Local S
Matches 131
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                                                                                                                                                                              Similarity
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                                    TSNRATGIPARESGSGSGTDETLSISSLEPEDEAVYYCQQRENWPWTFGQGTKVEFKRTV 130
                                                                                                          LLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRLLIYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPWTFGGGTKLEIKRADAAPTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSV 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELVMTQSPLSLSVSLGDQASISCRSSQSLVHTNGNTYLHWYLQKPGLSPKLLIYIVSNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRGEC
                                                                                                                                                               Conservative
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59.88;
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'
                                                                                                                                                           Score 702.5; DB
Pred. No. 1.6e-41
7; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 702.5;
Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                            February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                            06-Jan-1995 #text_change 11-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.6e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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C;Comment: This catalytic antibody has peroxidase oxidase. It is directed C;Superfamily: immunoglobulin V region; immunoglobulin homology F;16-94/Domain: immunoglobulin homology <IMM>
                                                                                    R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguo Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A;Title: Structural characterization of mouse monoclonal A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: JC5810
                                                                                                                                                                          monoclonal antibody 13-1 light chain - mouse
C;Speckes: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: JC5810
                                                   A; Molecule type: protein A; Residues: 1-218 < AKA>
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Best Local :
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A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
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R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region (Mabl3-1) - mouse (fragment)
N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.;
submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an a
A;Reference number: S68241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 'NI', 3-212 <TAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-218 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                    77 GIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSVF 136
                                                                                                                                                                                                                                                                                                                              Similarity
STLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                            IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS
                                                                                                      IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                        GVPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVS
                                                                                                                                                                                                                                                                                                 ELVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLATNLES
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61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                     Score 702; DB 2;
Pred. No. 1.7e-41;
2; Mismatches 49
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Yamaguchi, H.; Kamachi, M.;

Harada, porp

against a

Matches

Conservative

30; Mismatches

Query Match Best Local Similarity

56.9%;

Score 696; DB 2; Pred. No. 4.4e-41;

Length 218

Indels

4.

Gaps

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Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Accession: PLO106
C;Accession: PLO106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secr.
A;Reference number: PLO106; MUID:89235583; PMID:2541221
A;Accession: PLO106
A;Molecule type: mRNA
A;Residues: 1-144 <SIL>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-115/Domain: V region <VRE>
F;36-110/Domain: immunoglobulin homology <IMM>
F;44-54/Region: complementarity-determining 1
F;70-76/Region: complementarity-determining 2
F;109-115/Region: complementarity-determining 3
F;116-127/Domain: J region <JRG>
F;118-144/Domain: C region (fragment) <CRE>
Ig kappa chain V region (17/9) - mouse (C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C;Accession: A31790 Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; W.R.Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; W.J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data; Reference number: A92686; MUID:89034213; PMID:3182835
                                                                                                                                                                                               RESULT 15
A31790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 IVLTQSPATLSLSPGERATLACRASQTASR----YLAWYQQKPGQAPRLLIYDTSNRATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 IPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSVFI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEAPAQLLFLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
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                                                                                                                                                                                                                                                                                                                                                                                     GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEAPAQLLELLLHUPDTTGETVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 695; DB 2;
Pred. No. 3.4e-41;
4; Mismatches 7
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                                                                           Kenten, J.H.; Wilson,
                             and binding data for an
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A;Accession: A31790
A;Mclecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:C;Superfamily: immunoglobulin v region; immunoglobulin C;Reywords: heterotetramer; immunoglobulin F:16-96/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                           128;
                                                                                                                                            61
                                                                                                                                                                                                                                                     21 EIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAWYQQKPGQAPRLLIYDTSNR 74
                                                                                                                                                                                                                 1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTR 60
                                                                                                                                                                                                                                                                                                            Similarity
MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
                                LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                      VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEFQNGVLNSWTDQDSKDSTYS
                                                                                                                                            ATGIPARESGSGSGTDETLSISSLEPEDFAVYYCQQRENWEWTFGQGTKVEFKRTVAAPS 134
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                       56.8%; Score 695; DB 2; 58.2%; Pred. No. 5.3e-41; tive 38; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                             1; NID:g533234; immunoglobulin
                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                             Length 220
                                                                                                                                                                                                                                                                                                                                                                                                   PIDN:AAA39162.1; PID:g533235 homology
                                                                                                                                                                                                                                                                                           Indels
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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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          100.0
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2514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
    /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
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    /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
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    /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
    /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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    /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_EVB_FUB.pep:*
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  US-10-225-108A-3
US-09-848-832-3
US-09-848-832-3
US-09-82-6998-26
US-10-150-475A-6
US-10-127-694-5
US-10-227-694-5
US-09-726-258-71
US-09-748-429B-8
US-10-124-807-8
US-10-124-807-8
US-10-253-366-2
US-10-316-694-2
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2245.783 Million cell updates/sec
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Sequence 3, Appli
Sequence 21, Appl
Sequence 26, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 71, Appl
Sequence 71, Appl
Sequence 11, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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ALIGNMENTS

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US-10-25-108A-3

Sequence 3, Application US/10225108A

Publication No. US20030157112A1

Sequence 3, Application US/10225108A

Publication No. US20030157112A1

GENERAL INFORMATION:

APPLICANY: HOOPER, Craig

APPLICANY: HOOPER, Craig

APPLICANY: HOOPER, Craig

TITLE OF INVENTION: Recombinant Antibodies, and Compositions

TITLE OF INVENTION: Antibodies, and Compo
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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-848-832-3
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US-09-848-832-3
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Best Local
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                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/848,832
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                       KFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                              VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK 240
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Pred. No. 3.4e-165;
; Mismatches 0;
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; Sequence 21, Application US/
; Patent No. US20020131968A1
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Frewin, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: Waldmann
CURRENT APPLICATION NUMBER: US/09/736,371B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEO ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 21
RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449
                           DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                               PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV 439
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                                                                                                    PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
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Pred. No. 4.7e-149;
B; Mismatches 11;
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                                                                                     Sequence 6, Application US/10150475A publication No. US20030103985A1 GENERAL INFORMATION:
APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody FILE REFERENCE: 1/1211
CURRENT FILING DATE: 2002-05-17
PRIOR APPLICATION NUMBER: US 60/307,451
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/538,913
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
SEQ ID NO 26
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hoogenboom, Hendricus R.J.M.
APPLICANT: Henderikx, Maria P.G.
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DYX-015.1 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/822,698A CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: artificial sequence
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TYPE: PRT
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93.2%;
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Pred. No. 1.6e-147;
- ""sematches 12;
                                                                                                   Immunoconjugates
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-150-475A-6
                                                                ; OTHER INFORMATION: US-10-020-786-9
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US-10-020-786-9
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Query Match
Best Local Similarity
Matches 418; Conserv
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                                                                                                                                                            SEQ ID NO 9
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Best Local Similarity
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APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                 APPLICANT: Simmons, Laura C. APPLICANT: Klimowski, Laura
                                                                                                            ORGANISM: Artificial sequence
                                                                                                                              TYPE: PRT
                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
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                                                                             anti-TF heavy chain
              87.4%;
88.6%;
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              Score 2196;
Pred. No. 2.
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DB 15;
2.6e-143;
hes 37;
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Conservative

9;

Mismatches

Indels

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Gaps

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                                                                                                                                                                                                                           Query Match
Best Local S
Matches 418
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APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
FILE REFERENCE: p1867R1
CURRENT PPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US 60/315,209
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 470
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10227694 Publication No. US20030077739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                   FEATURE:
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                 183
                                              127
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                                           MIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 182
------FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 178
                                                                                                    FGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
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|------FDYMGQGTLYTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
             VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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Conservative
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pred. No. 2.6e-143;
9; Mismatches 37;
                                                                                                                                                                                                                                                    Length
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                                                                       ; TYPE: Am;
; TOPOLOGY:
US-09-726-258-71
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US-09-726-258-71
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                          Query Match
Best Local Similarity
                                                                                                    APPLICATION NUMBER: 60/094003
ETLING DATE: 24-ULI-1998
ATTORNEY_AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb |
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Genentech, Inc., Hsei, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                                                               FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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                          87.3%;
91.2%;
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               9;
             Score 2193.5;
pred. No. 3.7e
9; Mismatches
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; OTHER INFORMATION:
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LENGTH: 476
TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                Matches
                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
                                                                                                                                                                                                                                                                                                                           APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Simmons, Laura C. APPLICANT: Klimowski, Laura
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                                                                    GLEWVSAISA-SGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVHNAKTK 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGG--FDYWGQG
                                                       GLEWVGWINTYTGEPTYAAD-FKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAK--YP
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                                                                                                                                                                                                                                                                                                                                                            Reilly, Dorothea
                                                                                                                                                Conservative
                                                                                                                                                                                                    anti-VEGF heavy chain
                                                                                                                                                       87.0%;
88.8%;
                                                                                                                                                                                                                                                                                                    2002-03-26
                                                                                                                                              14;
                                                                                                                                            Score 2187; DB 15;
Pred. No. 1.1e-142;
4; Mismatches 35;
                                                                                                                                            Indels
                                                                                                                                                                   Length
                                                                                                                                              4.
                                                                                                                                              Gaps
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US-09-948-429B-8
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                     Best Loc
Matches
                                          Query Match
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                                                                            MOLECULE TYPE:
                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 699 Prince CITY: Alexandria
                                                                                                                                                                                                                                               FILING DATE:
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                                Local Similarity
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Sequence 8, Application US/09948429B Patent No. US20020177689A1
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DO
                                                                                                                                                                                                                                                                                NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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 Conservative
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TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THER
IMMUNOSUPPRESANTS"
               86.8%;
86.7%;
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18;
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Score 2183; DB 10;
Pred. No. 2.1e-142;
8; Mismatches 34;
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RESULT 11
US-10-124-807-8
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                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383
FILING DATE:
APPLICATION NUMBER: US 08/
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FO TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 699 Prince
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: 22314
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NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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699 Prince Street
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                                                                                                                            US 08/487,550
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US-10-124-905-8
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INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Anderson, Day
TITLE OF INVENTION: "MO)
TITLE OF INVENTION: TO I
TITLE OF INVENTION: PHAN
TITLE OF INVENTION: PHAN
TITLE OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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Best Local Sin
Matches 418;
                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/10124905 Publication No. US20020166136A1
            COUNTRY: USA
2IP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM
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                                                                                                                        STREET: 655
CITY: Alexandria
                                                                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                   699 Prince
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                   compatible
                                                                                                                                                                                                                                                                  , Darrell R.

"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THE
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  PC-DOS/MS-DOS
                                                                                                                                                                   Street
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Pred. No. 2
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Best Local Sim
Matches 418;
Sequence 2, Application US/10356974
Publication No. US20030153735A1
GENERAL INFORMATION:
APPLICANT: BREECE, TIMOTHY N.
APPLICANT: FAHRNER, ROBERT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                  477
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                                                                                                                                                                                                                                                                                                                                                                      VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                 GK 478
                                                                                                                                          GK 474
                                                                                                                                                                              QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                  GKGPEWVGFIRNKPNGGTTEYAASVKDRFTISRDDSKSIAYLQMSSLKIEDTAVYYCT--
                                                                                                                                                                   QPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP
                                                                                                                                                                                                                                                                                                                                 PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
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86.7%; Pred. No. 2
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2.1e-142;
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230

APPLICANT: BASEY, CAROL D.

APPLICANT: BLANK, GREG S.

TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/10/253,366
CURRENT FILLING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US/09/304,465
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 449 TYPE: PRT

RESULT 14 US-10-253-366-2

Sequence 2, Application US/10253366 Publication No. US20030078388A1 GENERAL INFORMATION:

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LENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 60/354,579
PRIOR FILING DATE: 2002-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: GORRELL, JEFFREY R.
APPLICANT: PHAM LAZZARESCHI, KATHLYN
APPLICANT: LESTER, PHILIP M.
APPLICANT: PENG, DAVID
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1939R1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
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SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
              SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473
                                                           VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                             VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP SNNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                         PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS HEDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                       PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS;#EDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                   GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK)YFPEPVTVSWNSGALTSGV
                                                                                                                                                                                                                                                                                                                                                  GQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVK)YFPEPVTVSWNSGALTSGV
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                                                                                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDR EVTMIVVLNGG-----FDYW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQA?GKGLEWVARIYPTNGYTRY
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Pred. No. 2.4e-142;
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Sequence 2, Application US/10316694

Publication No. US20030118583A1

GENERAL INFORMATION:
APPLICANT: EMERY, JEFFERSON C.
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: STABILIZING POLYPEPTIDES WHICH HAVE BEEN EXPOSED TO UREA FILE REFERENCE: P1940R1

CURRENT APPLICATION NUMBER: US/10/316,694

CURRENT APPLICATION NUMBER: US 50/341,891

PRIOR APPLICATION UNUMBER: US 60/341,891

PRIOR FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 449

TYPE: PRT
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Artificial sequence; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-10-253-366-2
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                                                                                                                   ; OTHER INFORMATION: US-10-316-694-2
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US-10-316-694-2
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Best Local Similarity 90.6
Matches 416; Conservative
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EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY 60
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                                                            Conservative
                                                                                                                               Sequence is synthesized
                                                                        90.6%;
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                                                       Score 2181.5; DB 15; Length 449; Pred. No. 2.4e-142; 8; Mismatches 20; Indels 15;
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Pred. No. 2.4e-1
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e-142;
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	S -	411	Db
	5 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473	435	Qy
410	VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	351	da
434	VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	375	ОУ
350	1 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 350	291	ДĎ
374	KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ	315	ν
290	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	231	Db
314	PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA	255	Qy
230	HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCP	171	da
254	HTEPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP	195	УО
170	1 GQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 170	111	Дb
194	GQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV	135	Qγ
110	61 ADSVKGRETISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGEYAMDYW		מם
134	DREVIMIVVLNGGFDYW		Qy

Search completed: September 12, 2003, 13:06:06 Job time: 32.7966 secs

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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein - protein search, using sw model
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      100.0
100.0
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ALIGNMENTS

RESULT 1 AAO14066 ID CARREST CONTRACTOR HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain; human monoclonal rabies virus neutralising antibcdy; immunoglobulin; light chain; central nervous system; CNS; prophylactic therapy; clone JA. (UYJE-) UNIV JEFFERSON THOMAS 16-MAY-2000; 2000US-204518P. 04-MAY-2001; 2001WO-US14468. 22-NOV-2001. WO200188132-A2 Homo sapiens. Light chain protein of the monoclonal antibody from clone JA 07-MAY-2002 AAO14066; AA014066 standard; Protein; (first entry) 234 A

WPI; 2002-062381/08 N-PSDB; AAK98702.

Hooper DC,

Dietzschold B;

Novel isolated human monoclonal rabies virus neutralising antibody

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RESULT 2
ABUO8018
ID ABUO
XX ABUO
XX ABUO
XX Huma
XX Patl
XX Patl
XX Patl
XX I Hool
XX Hool
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Best Local :
   N-PSDB;
                                                    Hooper DC,
                                                                                                                                                                                                                                                                                               Human; antibody; constant region; monoclonal antibody 57; Matiable region; Rabies; neurological disease; infection central nervous system; rabies virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the light chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rabies virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified sway from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for treating an individual exposed to a rabies virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious post exposure prophylactic therapy for individuals exposed to a rabies virus.
                                                                                      (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                              WO2003016501-A2
                                                                                                                                                                                                                                                                                                                                                                                        Human monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating individual exposed to rabies virus and for preventing spread of rabies virus to central nervous system -
                                                                                                                       21-AUG-2001;
                                                                                                                                                       21-AUG-2002; 2002WO-US26584.
                                                                                                                                                                                            27-FEB-2003
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                                                    Dietzschold
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Pred. No. 5.5e-70;
Pred. No. 5.5e-70;
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RESULT 3
AAY92239
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XX AAY9
XX AAY9
XX 10-A
XX BONE
KW BONE
KW BMDS
KW anti
XX HOME
CX HOME
CX HOME
FT MOOD!
FT MOOD!
FT MOOD!
FT MOOD!
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention discloses a recombinant antibody comprising a constant cregion of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable cregion. Rables is an acute, neurological disease caused by infection of the central nervous system with the rables virus, a member of the Lyssavirus genus of the family Rhabdowiridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid molecule encoding the antibody, and isolating the recombinant antibody camping the recombinant antibody campitated and treating an individual exposed to a pathogen by camping to the individual the recombinant antibody. The recombinant cantibodies are useful for preventing (vaccine) and treating an individual exposed to a pathogen, e.g. rables infection. They are also useful for the gualitative and quantitative determination of the rables virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                  Bone marrow-derived serum protein; immunoglobulin kappa light chain; BMDSP-1; cytostatic; anti-HIV; antiasthmatic; antiatherosclerotic; anti-inflammatory; antiarthritic; antisclerotic; hypotensive; antivi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New recombinant antibody comprising a constant region of Mab 57 linked to a non-Mab 57 variable region, useful for treating an individual exposed to a pathogen, e.g. rables infection
                                                                                    Modified-site
                                                                                                                                                                      Homo
                                                                                                                                                                                                      antiparasitic
                                                                                                                                                                                                                                                                                          Human bone marrow-derived serum
                                                                                                                                                                                                                                                                                                                          10-AUG-2000
                                                                                                                                                                                                                                                                                                                                                             AAY92239;
                                                                                                                                                                                                                                                                                                                                                                                             AAY92239 standard;
                   Modified-site
                                                                                                                   Modified-site
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36..11(
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"potential protein kinase C phosphorylation site"
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                                                                                                                                                                                                                                                                                         protein
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Best Local (
                                                                                                                                                                    Human bone marrow-derived serum proteins (BMDSP) 1 has chemical and structural similarity with immunoglobulin kappa light chain. BMDSP-1 and BMDSP-2 are useful for treating or preventing a disorder associated with decreased expression or activity of BMDSP.

Antagonists of BMDSP are useful for treating or preventing a disorder associated with increased expression or activity of bone marrow-derived serum proteins. The disorders include cancers (melanoma, adenocarcinoma, sarcoma), immune disorders (acquired immunodefictency syndrome (AIDS), asthma, atheroscierosis, Crohn's disease, bronchitis, multiple sclerosis, osteo- and rheumatoid arthritis), viral infections, parasitic infections (schistosoma, tapeworm), and vascular disorders (arteriosclerosis, broaterosis, coultrie).
                                                                                                                                                                                                                                                                                                                  Claim
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            GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ
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AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted protein genes, and AAG712319 represent the proteins they encode. AAG71320-AAG71301 represent the proteins they encode. AAG71320-AAG71301 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, arms anteriamana discasses for rhenmatid arthritis, inflammation.

New nucleic acid molecule encoding a human secre:ed protein, usefu preventing, treating or ameliorating medical conditions such as rheumatoid arthritis, Alzheimer's disease and mirrobial infections

useful

Page 498-499; 581pp;

English

N-PSDB;

AIDS, autoimmune diseases (e.g., rheumatoid arthritis), infla allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, as skin disorders (e.g., psoriasis), sepsis, diabetes, atherosol cardiovascular disorders, angiogenic disorders, kidney disorders

atherosclerosis

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RESULT 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrine disorder; infection; wound healing;
cell culture; chemotaxis; food additive;
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disorder; tumour
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25-APR-2000;
21-DEC-2000;
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                                                     Rosen CA,
                                                                                                                                                                                                                                                                         12-APR-2001;
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immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
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No. 4.8e-64;
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Hanson DC,
Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                         Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft reject proliferative disorder; cancer; immunodeficient disorder.
                                                                          (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                               23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
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           23-DEC-1998;
                                  23-DEC-1999;
                                                                                    WO200037504-A2
                                                                                                                         Peptide
                                                                                                                                                               Homo
                                                                                                                                                                                       proliferative
                                                                                                                                                                                                Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFG
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          98US-0113647
                                   99WO-US30895
                                                                                                                                                                                                                                       of
                                                                                                                                   Location/Qualifiers
                                                                                                             /note-
                                                                                                                                                                                                                                       immunoglobulin clone 4.1.1
                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.6%;
91.5%;
                                                                                                           "signal peptide"
                                                                                                                                                                                        cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1108.5; DB Pred. No. 9.5e-63;
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RESULT 8
ABP71366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                           Key
                                                                                                 Mus musculus
                                                                                                                    antiarthritic;
                                                                                                                                Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
                                                                                                                                                      Anti-OPGL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                    Region
                                        Region
                                                                                                                                                                            28-APR-2003
                                                                                                                                                                                                  ABP71366;
                                                                                                                                                                                                                        ABP71366 standard;
                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for treating,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 AA;
                                                                                                                                                     antibody kappa light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                    cytostatic;
                    /note= "v
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                                                                        Location/Qualifiers
          /note=
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                                                                                                                                                                                                                        Protein;
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                                                  "IgG2
         "constant region"
                               "variable
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                                                                                                                      OPGL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1108.5; DB 21; Pred. No. 9.5e-63; 7; Mismatches 12; 1
                                                    signal peptide"
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                                                                                                                    anti-OPGL-1; artibody
                              region"
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Best Local
                                                                                  The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, is also useful for treating osteopenic disords an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a partient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's evadoroms or acromosals) of contents of the contents of 
  hyperimmunity proliferative
                                Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, menkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia
                                                                                                                               03-OCT-2000
                                                                                                                                                                                                               AAY93708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                 QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
                                                                             chain of immunoglobulin clone 6.1.1.
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    disorder;
disorder;
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  autoimmune
cancer; im
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Pred. No. 3.5e-62;
6; Mismatches 13
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  ine disease; diabetes; gra
immunodeficient disorder
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                   graft rejection;
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Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

disease; diabetes; graft rejection;

hyperimmunity disorder; autoimmune

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RESULT 10
AAY93733
ID AAY93
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AC AAY93
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DT 03-OC
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Best Local S
Matches 213
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                                        The kappa chain of
                                                                        03-OCT-2000
                                                                                                                                     AAY93733
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                                                                                                                                     standard;
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                                                                                                                                                                                                                                                                        GTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
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                                                                                                                                     Protein;
                                          immunoglobulin clone 6.1.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.6%;
91.0%;
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                                                                                                                                     234
                                                                                                                                                                                                                                                                                                                                                                                                                                                        6,
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Pred. No. 5.8e-62;
6; Mismatches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21;
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chain sequences,
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RESULT 11
AAR52951
ID AAR52
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AC AAR52
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DT 25-MA
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Best Local Similarity
Matches 213; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytofoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
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Peptide
   25-MAR-2003
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                                       AAR52951;
                                                                         AAR52951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)-4 containing specified heavy and light chain sequences, useful for treating, e.g. immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
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DB; AAA46897.
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                                                                         standard;
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                                                                                                                                                                                                                                                         GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                                                                                                                                                                            GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ
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(updated)
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Pred. No. 5
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5.8e-62;
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RESULT 12
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AC AAY93
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DT 03-OC
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                    03-OCT-2000
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Query Match
Best Local
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Yoshida
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(Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human monoclonal anti-IgE peptide antibody - inhibits histamine release from mast cells by allergen stimulation, useful for preventing allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 12; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB;
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)B; AAQ71872.
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                                                                              GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                                                       MEAPAQLLFLLLLWLPDTTGEIVMTQSPATLSVSPGGRAALSCRASQSVSNNIAWYQQKP
                                                                                                                                                                                                       MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
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                                                                                                                                                                                                                                                                                                                    234 AA;
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/label= light chain variable region
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                                                                                                                                                                                                                                                                  89.1%;
89.3%;
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                                                                                                                                                                                                                                                    10;
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Pred. No. 1.4e
10; Mismatches
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L.4e-61;
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standard;

Protein;

233 AA

(first entry)

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RESULT 13
AAY93731
ID AAY93
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AC AAY93
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DT 03-00
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Best Local S
Matches 213
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  03-OCT-2000
                         AAY93731;
                                             AAY93731 standard;
                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3;
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Corvalan JR;
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                                                                                                     ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                   GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                                                                                                                            MEAPAQULFILLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 1B;
                                                                                                                                                                                                                                               METPAQLLFLLLLMLPDTTGEIVLTQSPGTLSLSPGERATLSCRTS-VSSSYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain
                                                                                                                                                                                                                                                                                                                                               233 AA;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neveu MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0113647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157pp;
                                              Protein;
entry;
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                                                                                                                                                                                                                                                                                                            88
91
                                                                                                                                                                                                                                                                                                           .0%;
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                                              233
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                                                                                                                                                                                                                                                                                             Score 1085.5; DB 21;
Pred. No. 2.7e-61;
5; Mismatches 15; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              田
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g cytotoxic and light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-lymphocyte antigen chain sequences, use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gilman
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SC,
                                                                                                                                                                                                                                                                                                                     233;
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Best Local
                                                                                                                                                                                                                                                                                The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Peptide
                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune shyperimmunity disorder; autoimmune disease; diabetes; graft proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanson DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kappa chain
180
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DB; AAA46895.
                                                                                                                                                                                                          al Similarity
213; Conserv
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                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Fig 22k; 157pp; English.
                                                               GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
             ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                   GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                       METPAQLLELLLULPDTTGEIVLTQSPGTLSLSPGERATLSCRTS-VSSSYLAWYQQKP
                                                                                                                                                                       MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JR;
                                                                                                                                                                                                                                                             233 AA;
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0113647
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1..20
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                                                                                                                                                                                                                      88.8%;
91.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller
                                                                                                                                                                                                         5;
                                                                                                                                                                                                                     Score 1085.5; DB 21; Pred. No. 2.7e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EE,
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytotoxic T-lymphocyte antigen and light chain sequences, use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful
233
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RESULT 14 AAR12128

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                                                                                                       Query Match
Best Local :
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See also AAQ11879 and AAQ11880.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Peptide
                                                                                                                                                                                                                                                                                                                                                     Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                   Example 5; Fig 16; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           Shuford WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIBB CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgG aberrant light chain with duplicated variable region
                                                                                                                                                                                                                                                                                                                                                                                                      1991-163947/22
 61
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lobulin G; light chain; variable region; duplication;
immunity; group B streptococci.
MEAPAQLLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                          349
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Harris
                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0432700.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90WO-US06426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= variable region
/note= "L'V 1"
131...243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= constant region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= variable region
/note= "L'V 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                      88.5%;
63.6%;
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                                                                                                      Score 1082.5; D
Pred. No. 6e-61;
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                                                                                           Mismatches
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                                                                                 Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of
                                                                                                                                                                    07-NOV-1989;
                                                                                                                                                                                                                                                                                                                        Key
                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
01-AUG-1991
                                                                                                                                   Shuford
                                                                                                                                                                                   06-NOV-1990;
                                                                                                                                                                                                     16-MAY-1991.
                                                                                                                                                                                                                      WO9106305-A.
                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                        immunoglobulin passive immunit
                                                                                                                                                                                                                                                                                                                                                                                  181 IgG aberrant light chain with duplicated variable region
                                                                                                                                                                                                                                                                                                                                                                                                                            AAR13111;
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13111
                                                          Example
                                                                                                                                                   (BRIM)
                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                   1991-163947/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186
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                                                         5
                                                                                                          AAQ11878
                                                                                                                                   WW,
                                                                                                                                                    BRISTOL-MYERS
                                                                                                                                                                                                                                                                                                                                                       immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QDSKDSTYSLSSTLTLSKADYEKHKYYACEVTHQGLSSPYFKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKYQWKVDNALQSGNSQESVTE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTKVEIKHTTGEIVLTQSPATLSLSPGERATLSCRASQ 3VGSYLAWYQQKPGQAPRPL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYY.QHRDNWPPGATFGGGTKVE
                                                        Fig
                                                                                                                                  Harris
                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
                                                        16; 104pp;
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                                                                                                                                                                                                                                                                                                /label= leader peptide
18..130
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                      /label= variable
/note= "L'V 2"
                                                                                                                                                                                                                                                                              /label= variable region
/note= "L'V l"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                   Ę
                                                                                                                                                    SQUIBB
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                                                        English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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This sequence is deduced from the cDNA clone 4B9 Vk15 and includes the amino acid sequence beyond the first stop cocon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met

is given. Antib aberrant light

Antibody molecules of the invention light chains containing a duplicated

include one or

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Search completed: September 12, 2003, 13:00:41 Job time: 41.9915 secs
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                                                                                                                                                                                                                                                                                                     Query Match 88.5%;
Best Local Similarity 63.6%;
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                   produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta.

See also AAQ11879 and AAQ11880.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                               Sequence
                                        126
                                                                                                                                                    116
                                                                                    241
                                                                                                                           181 IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHRDNWPPGATFGGGTKVE
                                                                                                                                                                     121 GGGTKVEIKHTTGEIVLTQSPATLSLSPGERATLSCRASQSVGSYLAWYQQKPGQAPRPL 180
                                                                                                                                                                                             116
                                                                                                                                                                                                              414 AA;
                                                                                                                                                                                                                                                                                                    Score 1082.5; DB 12; Length 414; Pred. No. 7.1e-61; 3; Mismatches 9; Indels 115;
                                                                                                                                                                                                                                                                                                     Indels 115; Gaps
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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                       US-09-848-832-3
2514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100%
                  US-08-157-101A-7
US-09-027-449-71
US-09-027-449-71
US-09-121-952A-71
US-09-121-952A-71
US-09-121-952A-71
US-09-234-40A-71
US-09-526-098-8
US-09-526-098-8
US-09-526-0148-2
US-09-680-148-2
US-09-168-1531-8
US-09-168-1531-8
US-09-168-207C-18
US-09-296-005-18
US-09-282-846-2
US-09-282-846-2
US-09-887-352B-14
US-09-887-352B-14
US-09-168-145-2
US-09-168-145-2
US-09-168-145-2
US-09-168-145-2
US-09-168-145-2
US-09-169-207C-14
US-09-109-207C-14
US-09-109-207C-14
US-09-109-207C-14
US-09-109-205-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (without alignments)
748.902 million cell updates/sec
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                                                                                                                                                                                                                                                                                                               Sequence 7, Appli
Sequence 71, Appl
Sequence 71, Appl
Sequence 71, Appl
Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 18, Appli
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                                         sequence
                    8, Appli
2, Appli
2, Appli
2, Appli
3, Appli
8, Appli
18, Appli
19, Appli
10, Appli
114, Appli
114, Appli
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114, Appli
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US-08-157-101A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/08157101A Patent No. 5808032 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NAPPLICANT: NAPPLICANT: 7APPLICANT: 1APPLICANT: 1APPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION TITLE OF INVENTION: PLASMIDS THEREFOR
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4 5	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30	29	28
2037	2037	2044.5	2046	2046	2060	2062	2062	2086.5	2089	2090.5	2092	2092	2094.5	2100.5	2100.5	2104.5	2113
81.0	81.0	81.3	81.4	81.4	81.9	82.0	82.0	83.0	83.1	83.2	83.2	83.2	83.3	83.6	83.6	83.7	84.0
451	451	453	476	476	472	472	472	446	449	473	476	476	467	711	468	467	443
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US-09-466-635-3	US-09-247-352-3	US-09-301-593-18	US-09-526-098-4	US-08-487-550-4	US-09-301-593-30	US-09-301-593-43	US-08-793-450-8	US-08-397-411-7	US-08-458-516-13	US-09-049-672A-4	US-09-526-098-12	US-08-487-550-12	US-09-049-672A-8	US-09-485-737B-90	US-09-485-737B-67	US-08-704-744-81	PCT-US96-13152-4
Sequence 3, Appli	Sequence 3, Appli		Sequence 4, Appli	Sequence 4, Appli	Sequence 30, Appl		Sequence 8, Appli	Sequence 7, Appli	Sequence 13, Appl	Sequence 4, Appli	Sequence 12, Appl	Sequence 12, Appl	Sequence 8, Appli	Sequence 90, Appl	Sequence 67, Appl		Sequence 4, Appli

ALIGNMENTS

MATSUKURA, SHIGH TSURUOKA, NOBUO NISHIHARA, TATSURO

SHIGEKAZU

KURIHARA, TATSUYA

ARIMA, KENJI

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US-08-157-101A-7
Query Match
Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                                                                                              ZIF: 2005
ZIF: 2005
ZIF: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                   LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEERA: 202-82-0944
TELEX: 6714627 CUCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100 NEW YORK AVENUE, N.W.
           Conservative
                           88.4%; Score 2221.5;
89.9%; Pred. No. 2.1e
           19;
           Mismatches
                             .1e-172;
                                             DB 1;
                                             Length 459;
           5
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1;

115

137 60 79

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RESULT 2
US-09-027-449-71
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                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/038,664
FILING DATE: 21-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: 101085R3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                SOFTMARE: WINPATIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA Way
CITY: South San Fr:
STATE: California
COUNTRY: USA
ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/027,449 FILING DATE: 20-Feb-1998 CLASSIFICATION: 435
TELEFAX:
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5. 6025158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGG
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US-09-026-985-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 71, Application US/09026985 Patent No. 6133426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity Matches 417; Conserv
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
            ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     STREET: 1 DNA Way
CITY: South San F
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 452 amino acids TYPE: Amino Acid TOPOLOGY: Linear
                                              APPLICATION NUMBER: FILING DATE: 20-Fe
                              CLASSIFICATION:
                                                                                                                                                                                       ZIP: 94080
                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLLESGGGLVQPGGSLRLSCAASGFTESNYAMSWVRQAPGKGLEWVSAISASGHSTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGG--FDYWGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGD-----YRYNGDWFFDVWGQG
                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                           Genentech,
                                              20-Feb-1998
                                                                                                                                                                                                                                         Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.3%;
91.2%;
                                                                US/09/026,985
                                                                                                                                                                                                                                                                           Inc.
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Pred. No. 3.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                   floppy
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                                                                                                                                                                                                                                                     Sequence 71, Application US/09121952A Patent No. 6458355
GENERAL INFORMATION:
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Best Local :
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
COMPUTER: IBM PC compatible
                                                                                                                                APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER (
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
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TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
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                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                STREET: 1 DNA Wa
CITY: South San
STATE: Californi
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mes 417; Conserv
                                         ZIP: 94080
                                                   COUNTRY:
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                                                                                                          ADDRESSEE:
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                                                                                            1 DNA Way
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ilarity 91.2%;
Conservative
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                                                                               Francisco
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Leonard G.
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                                                                                                        Inc.
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Pred. No. 3.8e-170;
9; Mismatches 24;
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           RESULT 5
US-09-234-340A-71
US-09-234-340A-71
; Sequence 71, Application US/09234340A
; Patent No. 6468532
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, V.
APPLICANT: Leong, Steven R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
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APPLICANT:

Inc., Hsei, Vanessa

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REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER:
FILING DATE: 20-FEB-
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APPLICATION NUMBER:
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                                                        LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENIYKTTPPVLDSDGSFFLYSKL
                                                                                                                 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPIPIEKTISKAKGQPREPQVYT
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INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: Line
234-3/0
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
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STATE: Californi
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                                                                                                                                                                                                                                                                                                                       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGG--FDYWGQG 137
                                                                                                                                                                                                                                                                                                                                                                                   EVQLLESGGGLVQPGGSLRLSCAASGETFSNYAMSWVRQAPGKGLEWVSAISASGHSTYL
                 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 437
                                                                                                                                                                                                                                                                                                        NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDWFFDVWGQG
LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                      APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
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                                                                                                                                                                                                                                                                                                                                                                   EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY
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1 DNA Way
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91.2%;
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Pred. No. 3.8e-170;
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US-08-487-550-8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,03
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LENGTH: 478 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
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STATE: VA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenth Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                    REVTMIVVLNGG------FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL 172
                                                                                                                                                                                                                              GKGLEWVSAI--SASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD 118
                                                                                                                                                                                                                                                                       MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
                                                                                                                                                                                                                                                                                         MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                          PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                        VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
                                                                                                                                                    --TSYISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                              PSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
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86.7%;
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FC PHARMACEUTIAL COMPOSITIONS CONTAINING,
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Pred. No. 2
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                                                                                         Query Match
Best Local Similarity
Matches 418; Conser
                                                                                                                                                                                                                        NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                               TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US 08
FILING DATE: 07-JUN-1995
ATTORNEY FACENT INFORMATION:
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TITLE OF INVENTION:
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CITY: AL
STATE: V
COUNTRY:
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)9 Prince Street
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07-JUN-1995
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
                                                                                      86.8%; Score 2183; I
86.7%; Pred. No. 2.96
tive 18; Mismatches
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                                                                                      DB 4;
2.9e-169;
nes 34;
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APPLICANT: BASEY, CAROL D.

APPLICANT: BLANK, GREG S.

TITLE OF INVENTION: PROTEIN PURIFICATION

FILE REFERENCE: P1241R1D2

CURRENT APPLICATION UNMERR: US/09/679,397

CURRENT FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                   SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09679397 Patent No. 6339142
                                                                                                                                                                                         Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                          LENGTH: 44
TYPE: PRT
                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                            ORGANISM: Artificial sequence
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Pred. No. 3.56
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; OTHER INFORMATION:
; Patent No. 6417335
US-09-680-148-2
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APPLICANT: BLANK, GREG S.

TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1D1
CURRENT APPLICATION UNMBER: US/09/680,148
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
PRIOR FILING DATE: 1998-05-06
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Best Local :
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PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
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TYPE: PRT
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                                     KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
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Pred. No. 3.5e
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APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/09/304,465A
CURRENT TILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 2
SEQ ID NOS: 2
                                    RESULT 11
US-08-466-151-8
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; OTHER INFORMATION:
; Patent No. 6489447
US-09-304-465A-2
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Patent No. 6489447
            Sequence 8, Application Patent No. 6037453
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GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial sequence
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Pred. No. 3.5e-169;
8; Mismatches 20;
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Best Local
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APPLICATION NUMBER: 08/4UDDI/
FILING DATE: 15-MAR-1995
PRIOR APPLICATION DATA: 08/185899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-Jun-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
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CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
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CITY: South San F
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Amino Acid
TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Svoboda, Craig G. REGISTRATION NUMBER: 39,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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                                  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                      PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKT
                                                                                                       FPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPC
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                                                                                                                                                                                                                                                                                                                                                                         86.6%; Score 2178; DB 3; 90.8%; Pred. No. 6.9e-169; tive 14; Mismatches 20;
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US-08-466-163B-8
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CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405,617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185,899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/879,495
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR APPLICATION NUMBER: US 07/744,768
PRIOR FILING DATE: 1991-08-14
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LENGTH: 453
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APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P0718p2C1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 64
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                                                                                                                                                                  PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHI:DPEVKFNWYVDGVEVHNAKT
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LTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK .174
                                 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEHNYKTTPPVLDSDGSFFLYSK
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                                                                                                   KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALI'APIEKTISKAKGQPREPQVY
                                                                                                                   KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALIAPIEKTISKAKGQPREPQVY
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Pred. No. 6.9e-169;
4; Mismatches 20;
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US-08-887-352B-18
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                   Best Local Sim Matches 414;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: SVODOda, Craig G.
REGISTAGE 39,044
REGISTAGE NUMBER: 91,044
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-U1-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Improved Anti-IgE Antibodies
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
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                                  LADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFDYWGQGT 138
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
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90.8%;
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Pred. No. 1.7e-168;
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LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
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US-09-109-207C-18
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            Sequence 2, Application Patent No. 6194551 GENERAL INFORMATION:
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Best Local Similarity
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  APPLICANT:
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Pred. No. 1.7e-168;
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APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu,
TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Im
FILE REFERENCE: P1123r1
CURRENT APPLICATION NUMBER: US/09/109,207C
CURRENT FILING DATE: 1998-06-30
PRIOR APPLICATION NUMBER: US/09/1051,554
PRIOR FILING DATE: 1997-07-03
NUMBER OF SEQ ID NOS: 44
                                                                                                                                                    PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP
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                                                                                             REEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTL
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: LENGTH: 451
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Artificial Sequence
: LOCATION: 1-451
: OTHER INFORMATION: Sequence is completely synthesized
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Search completed: September 12, Job time: 28.7797 secs
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FILE REFERENCE: 91266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
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Matches 414; Conserv
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                                                                                                                                              VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
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sp_bacteria:*
sp_fungi:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_rodent:*
sp_virus:*
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                  1 Q8NF17
Q8NF17
1 Q91Z05
1 Q9R1A4
1 Q9D8L4
1 Q9D8L4
1 Q99L31
1 Q99L31
1 Q99L31
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1 Q99L35
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1 Q99
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Q8TC63
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Q9184 mus
Q99124 mus
Q99131 mus
Q99131 mus
Q99136 mus
Q873h6 mus
Q873h6 mus
                  Q96pq8
Q96bb9
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26.8	27.0																										
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Q91WR1	Q8K0F2	Q96KX8	Q8K0Z4	Q8K172	Q96DK0	Q91X92	Q91WT1	Q99LA6	Q8WY24	Q9BRV0	Q96AA6	Q8WUX4	Q96EY0	Q9BQB8	Q96GA6	Q921K1	Q9BU10	Q8VCX7	Q8WU38	Q8VEA0	Q91XE1	Q91Z07	Q91WP5	Q99KA4	Q8NCL6	Q8N5K4	Q96K68
Q8vcx4 mus i	mus	homo		Q8k172 mus i	_	Q91x92 mus :	Q91wt1 mus ı	6 mus	Q8wy24 homo :	Q9brv0 homo :	homo	homo	Q96ey0 homo :	homo	homo	Q921k1 mus i	homo	mus	Q8wu38 homo :	0 mus	Bum	Q91z07 mus r	Bum	Q99ka4 mus r	homo	Q8n5k4 homo:	Q96k68 homo :
musculu	musculu	sapien	musculu	musculu	sapien	musculu	musculu	musculu	sapien	sapien	sapien	sapien	sapien	sapien	sapien	musculu	sapien	musculu	sapien	musculu	musculu	musculu	musculu	musculu	sapien	sapien	sapien

ALIGNMENTS

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QRTC77

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AC QRTC

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Best Local S
Matches 438
                                                                                                                                                                                                                                                  Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

R EMBL; BCC24289; AAH24289.1; -

R InterPro; IPR007110; IJ-11ke.

R InterPro; IPR003006; IJ-MHC.

R InterPro; IPR003596; IJ-V.

R INTERPRO; IFR003596; IJ-V.

R Pfam; FP00047; IG; 4.

R PROSITE; PS0035; IG_LIKE; 4.

R PROSITE; PS00290; IG_MHC; 2.

W Hypothetical protein.

SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E C:C64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8TC77 PRELIMINARY; PRT; 4/1 AA.
Q8TC77;
Q1-UUN-2002 (TrEMBLrel. 21, Created)
O1-UUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
61 GKGLEWVSSMSSSSSYIYYADSVKGRFTISRDNAKNSLYL/)MNSLRAEDTAVYYCARDLR 120
                      61 GKGLEWVSAISASGHSTYLADSVKGRPTISRDNSKNTLYL/)MNSLRAEDTAVYYCAKD-R 119
                                                                                                                                                                                     Similarity
                                                                                 Conservative
                                                                                                                                                                     92.5%; Score 2325.5; DB 4; Length 471;
92.2%; Pred. No. 2.2e-183;
tive 19; Mismatches 13; Indels 5;
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Best Local S
Matches 404
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Q8N4Y9;
Q1-OCT-2002 (TrEMBLrel. 22, Cres
Q1-OCT-2002 (TrEMBLrel. 22, Last
Q1-MAR-2003 (TrEMBLrel. 23, Last
Q1-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein
Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; C1
Mammalia; Eutheria; Primates; C1
                                                                                                                                                                                                                                                                                                       Submitted (JUN-2002) to the EME Submitted (JUN-2002) to the EME EMBL; BC033178; AAH33178.1; -. InterPro; IPR003597; Ig_-11. InterPro; IPR003597; Ig_-01. InterPro; IPR003596; Ig_-wHC. InterPro; IPR003596; Ig_-v. Pfam; PF00047; Ig; 4. SMARP; SM00407; IGc1; 3. SMARP; SM00407; IGc1; 3. SMARP; SM00405; IGv. 1. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS50835; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Primary
Strausberg R.;
                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 521 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                      404;
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                                                                                                                                                                                                                                    Similarity
                                                                                        EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD
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                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                               57156 MW;
                                                                                                                                                                                                                                 83.8%;
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Last sequ
Last anno
                                                                                                                                                                                                                   Score 2105.5; DB 4
Pred. No. 3.6e-165;
6; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                               2AC7D22E72D6CAA2 CRC64;
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Best Local S
Matches 368
                                                                                                                                                                                                                                                                                                       Submitted (MAR-2002) to the EMBL, EMBL; BC025985; AAH25985.1; -. Interpro; IPR001923; BlueCu_1. Interpro; IPR0019023; BlueCu_1. Interpro; IPR003006; Ig_MHC. Interpro; IPR003006; Ig_MHC. Interpro; IPR003506; Ig_v. Pfam; pP00047; ig; 4. SMART; SM00406; IGV; 1. SMART; SM00406; IGV; 1. PROSITE; PS00196; COPPER_BLUE; 1 PROSITE; PS00196; COPPER_BLUE; 1 PROSITE; PS00290; IG_MHC; 3. Hypothetical protein. SEQUENCE 473 AA; 51986 MW; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TC63;
Q8TC63;
01-JUN-2002
01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N
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 184
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Primates;
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77.88;
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WLF--LVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASG--FTFSNYAMSWVRQAPGK
MIVVLNGGED-YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
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(TrEMBLrel. 21, Last seq
(TrEMBLrel. 23, Last ann
                                    -GFGAHWGQGKLVSVSPASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPV
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Pred. No. 8.7e
31; Mismatches
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                                                                                                                                                                               E29920B09BA369F5 CRC64;
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3.7e-147;
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Best Local S
Matches 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.;
Strausberg R.;
Stbmitted (MAR-2002) to the EMBL/GenBank/DDBJ date EMBL; BC024405; AAH24405.1; -
InterPro; IPR0037110; Ig-1ike.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003599; Ig_V.
InterPro; IPR003599; Ig_V.
INTERPOOAT, 1g; 4.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS05035; IG_MHC; 1.
R PROSITE; PS05035; IG_MHC; 1.
R PROSITE; PS05035; IG_MHC; 1.
R PROSITE; PS05035; IG_LIKE; 4.
R PROSITE; PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R3V9 PRELIMINARY; PRT; 469 AA. Q8R3V9; Q08R3V9; Q08R3V9; Q08R3V9; Q01-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 52.0 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                           DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP
                                                                           PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPSSIEK
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DPEVQFSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.1%; Score 1660.5; DB 11; Length 64.2%; Pred. No. 1.6e-128; tive 72; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      534793F155D05457 CRC64;
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; Murinae; Mus
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Best Local S
Matches 309
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SMART; SM00407; IGcl; 3.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2002) to the EMBL; AK090464; BAC03445.1;
                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Spleen;
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara.
"The nucleotide sequence of a long cDNA clone iso.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8NF17
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR007110;
InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                     NYKTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFSCSVMHIALHNHYTQKSLSLSPGK 474
                                          KGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKIJVDKSRWQQGNVFSCSVMH
                                                                   SGLYSLSSVVTVPSSSLGTQTYTCNVNHKPSNTKVDKRVEI.KTPLGDTTHTCPRCPEPKS
                                                                                                                                                                                      SGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EALHNRFTQKSLSLSP
          EALHNHYTQKSLSLSP
                                 KGFYPSDIAVEWESSGQPENNYNTTPPMLDSDGSFFLYSKITVDKSRWQQGNIFSCSVMH
                                                                                                                                           CDTPPPCPRCPEPKSCDTPPPCPRCPEPKSCDTPPPCPRCI'APELLGGPSVFLFPPKPKD
                                                                                                                                                                                                                                                                                                                                                                                                                                          ıs (Human).
Metazoa; Chordata; C
™ + heria; Primates; (
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                                                                                                                                                                                                                                                                                      AA; 56111 MW;
                                                                                                                                                   -----EPKSCDKTHTCPPCI'APELLGGPSVFLFPPKPKD
                                                                                                                                                                                                                                                                                                                                       Ig-like.
Ig_cl.
Ig_MHC.
                                                                                                                                                                                                                                                          64.7%;
82.2%;
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438
                                                                                                                                                                                                                                                 score 1625.5; pred. No. 1.4e; Mismatches
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Last annotation updat
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isolated from
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RESULT
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ID Q9207
AC Q92
DT Q90
DT Q90
OC Q90

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Best Local S
Matches 301
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O91205;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 20, Last sequence upda O1-MAR-2003 (TrEMBLrel. 23, Last annotation up Hypothetical 51.9 kDa protein.
Hypothetical 51.9 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verteb.
Mammalla; Eutherla; Rodentla; Sciurognathi; Mu.
NCBL_TaxID-10090;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 3
SMART; SM00406; IG; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00190; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010327; AAH10327.1; -.
MGD; MGI:2144967; AU044919.
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                                     474
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                                                                       VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
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473 AA; 5
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62.6%;
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Pred. No. 1.7e
70; Mismatches
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95;
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RESULT

Q9D8L4

PRELIMINARY;

PRT;

473

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RESULT 8
Q9D8L4
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Matches 288
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Q9R1A4;
Q1-MAY-2000 (TrEMBLrel. 13, C
Q1-MAY-2000 (TrEMBLrel. 13, L
Q1-MAR-2003 (TrEMBLrel. 23, L
Gammal heavy chain of Mab7 (F
IGH-4.
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NON_TER
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAX-1999) to the EMBL; R152372; AAD40243.1; HSSP; P01842; 7FAB MGD; MGI:96446; Igh-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust antibody (and 7, its light and heavy chains) and construction single chain antibody (scFV).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00047; ig; 4.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single chain antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                      :96446; Igh-4.; IPR007110; Ig-like.; IPR003006; Ig_MHC.; IPR003596; Ig_V.
                                                                  TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                           VLQSSGLYSLSSVYTYPSSSLGTQTYICNVNHKPSNTKYDKRYEPKSCDKTHTCPP--CP
                                                                                                                                                                                                                                                                                        VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                                                                                                                                                                                                                                                                                                                    DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFD-YWGQGTR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00290; IG_MHC;
                                                       NVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK
                                                                                                            LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                                         DSVKGRFTIYKDKDRNILSLQMSSLRSEDTAMYYCAR-----GDYSAYWGPGTL
                                                                                                  IPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKL
                                                                                                                                                                                                                                   VLQSD-LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG---
                                                                                                                                                                                                                                                                              VTVSAAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPA
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437 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                          61.3%;
63.0%;
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, Last annotation
(Fragment).
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RX MEDLINE-C108566; PubMed-11217851;
RX MEDLINE-C108566; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cosavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Asaski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
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Best Local S
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Mus musculus (Mouse).

Rukaryota; Metazoa; Chordata;

Mammalla; Eutheria; Rodentia;

MCBI_TaxID-10090;
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01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
1810060009R1k protein.
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Functional annotation of a full-length mouse cDNA collection."; nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
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rPro; IPR007110; I
rPro; IPR003006; I
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277; Conserv
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HEWSWVFLFLLSVTAGVHCQVQLKQSGAELVKPGASVKISCKASGYTFTDYYINWVKQRP
                                                             TKVDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCV
                                                                              TKVDKRVEPK-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                          VTMIVVLNGGFD----YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                                                                                     GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR---
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IPR003596; Ig_v.
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                                                                                                                                                                                         SGYDYDWFAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKG
                                                                                                                                                                                                                                                                                                                                                                           60.1%; Score 1511.5; DB 11
57.1%; Pred. No. 3.2e-116;
57.1%; Mismatches 100;
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Query Match
Best Local S
Matches 274
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS500290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; 1
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Q99LC4;
01-JUN-2001
01-JUN-2001
01-MAR-2003
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Similar to RIKEN cDNA 1810060009 gene.
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14; Conservative
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                                               KIVPRDCG---
                                                                                                VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                      YSYDL----FAYWGQGTLVTVSAAKTTPPSVYPLAPGS! AQTNSMVTLGCLVKGYFPEP
                                                                                                                                                                                                 GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYHLLSSLTSEDSAVYFCARSSY
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                                     EVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH(;DWLNGKEFKCRVNSAAFPAP
                                                                                                                                     VTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTVPSETVTCNVAHPASSTKVDK
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                                                                                    -CKPCICTVPEV---SSVFIFPPKPKDVITITLTPKVTCVVVDISKDDP
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57.6%; Pred. No. 6.6e-1
tive 85; Mismatches 1
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InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03096; Ig_v.
Pfam; PF00047; 1g; 3.
SMARP; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW; 9
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Submitted (FEB-2001) t
EMBL; BC003878; AAH038
HSSP; P01842; 7FAB.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN cDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                         TISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNT
                                                                                                                                                                                                        TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                         ISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIER
                                                                                                                                                                                                                                                                      PKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                                 TWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNTQPIMDTDGSYFIYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSHSPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                    IEKTISKTKGRPKAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001) to the AAH03878.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1474; DB 11; Pred. No. 4e-113;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96352328B3332ADB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 113;
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   RESULT 12
Q8R3H6
ID Q8R3H
AC Q8R3H
DT 01-JU
DT 01-JU
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Best Local S
Matches 274
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 3.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 4.
PR0SITE; PS50835; IG_MHC; 1.
SEQUENCE 473 AA; 52449 MW;
Q8R3H6;
Q8R3H6;
Q1-JUN-2002
Q1-JUN-2002
Q1-JUN-2002
Q1-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99L25 PRELIMINARY; PRT; 473 AA.
Q99L25;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence up
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL; BC003888; AAH03888.1; HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg
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                                                                                                                                                            SLSPGK
                                                                                                                                                                                                      MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
||:::||:||:||:|| |
||:||::::|| ||:|| |
|MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVN
                                                                                                                                                                                                                                                                                                                                                                                                        HKPSNTKVDKRVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GGSIYYGYGLYYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTMIVVLNGG-----FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALG
                                                                                                                                                                                                                                                                                                                                                                                         HPASSTKVDKKIEPRG-PTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPMVTC
 (TrEMBLrel.)
(TrEMBLrel.)
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                                                                PRELIMINARY;
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21,
23,
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Last
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                                Created)
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Pred. No. 7.56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE9889B7986DA155 CRC64;
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   sequence up
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Gaps

120 60 60

update)

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RESULT
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Q95M34
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Q95M36
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Best Local
                                                Q95M34 PRELIMINARY;
Q95M34;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                            01-DEC-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. Immunogobulin gamma 1 h
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Mammalia; Eutheria;
                    IGHC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical 51.7 kDa protein. Mus musculus (Mouse).
    Equus
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PS50835; IG_LIKE; 4.
PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                   TEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                                                                                                     PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                                                                                                                DLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGH
                                                                                                                                                                                                                                                                                                                                  ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                                                                                                                                           SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
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                                                                                                                PRELIMINARY;
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    (Horse)
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                                 1 heavy
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                                                19,
19,
23,
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                                Created)
Last sequence update)
Last annotation update)
chain constant region ()
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Pred. No. 3.6e-108;
'9; Mismatches 120;
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                                                                                                                337
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                                 (Fragment)
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Best I
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SMART; SM00407; IGC1; 2.

PROSITE; PS50835; IG_LIKE; 3

PROSITE; PS00290; IG_MHC; 2.

NON_TER 1 1
                                                                                              Q96PQ8 PRELIMINARY; PRT; 701 AA.
Q96PQ8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Pactor VII active site mutant immunoconjugate.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebratı;
Eukaryota; Metazoa; Chordata; Craniata; Vertebratı;
Mammalia; Eutheria; Primates; Catarrhini; Hominid;e
Hu Z., Garen A.;
"Targeting tissue factor on tumor vascular mouse models of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes. III. Alignment of c-mu, c
Immunobiology 199:105-119(1998).
EMBL; AJ300675; CAC44624.1; -.
                                MEDLINE=21477448;
Hu Z., Garen A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wagner B., Overesch G., Leibold W., Radbruch A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                              SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=9606;
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                                                   PubMed=11593034
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                                                                                                           Craniata; Vertebratı;
Catarrhini; Hominidae;
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SEQUENCE FROM N.A. MEDLINE=98383416; PubMed=9717671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Organization of the equine immunoglobulin
                                                                                                          PELLGGPSVFIFPPNPKDTLMITRTPEVTCVVVDVSQENPI)VKFNWYMDGVEVRTATTRP
                                                                                                                                                                             PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP);VKFNWYVDGVEVHNAKTKP
                                                                                                                                                                                                                      GFYSLSSMYTVPASTWTSETYICNVVHAASNFKVDKRIEP::PDNHQKVCDMS-KCPKCPA
                                                                                                                                                                                                                                   GLYSLSSVYTYPSSSLGTQTYICNVNHKPSNTKYDKRYEP-----KSCDKTHTCPPCPA
                                                                                                                                                                                                                                                                            ASTTAPKVFALAPGCGTTSDSTVALGCLVSGYFPEPVKVSIINSGSLTSGVHTFPSVLQSS
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                                                                                                                                                                                                                                                                                                                               Score 1263.5;
Pred. No. 5.8e
44; Mismatches
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Euteleostomi;

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Best Local S
Matches 230
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Interpro; IPRO001314; EGF_2.
Interpro; IPRO00188; EGF_1:
Interpro; IPRO00188; EGF_1:
Interpro; IPRO0188; EGF_1:
Interpro; IPRO0188; EGF_1:
Interpro; IPRO02383; GLA_blood.
Interpro; IPRO03597; Ig_c1.
Interpro; IPRO03597; Ig_c1.
Interpro; IPRO03096; Ig_MHC.
Interpro; IPRO03096; Ig_MHC.
Interpro; IPRO03094; VitK_dep_GLA.
Interpro; IPRO03094; VitK_dep_GLA.
Interpro; IPRO00294; VitK_dep_GLA.
Interpro; IPRO00109; IGGF_1:
Interpro; IPRO00109; IGGF_1:
Interpro; IPRO00101; EGFEDLOOD.
IPRINTS; PRO00101; EGFEDLOOD.
IPRINTS; PRO00101; EGFEDLOOD.
IPRINTS; PRO00101; EGF_CA; 1.
INTERPROVED SAS_HYDROXYL; 1.
INTERPROVED SAS_HYDROXYL; 1.
IPROSITE; PS000187; EGF_1; 1.
IPROSITE; PS001187; EGF_CA; 1.
IPROSITE; PS001187; EGF
Q96BB9 PRELIMINARY;
Q96BB9;
01-DEC-2001 (TrEMBLrel. 1:
01-DEC-2001 (TrEMBLrel. 1:
01-MAR-2003 (TrEMBLrel. 2:
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chord:
Mammmalia; Eutheria; Primai
NCBI_TaxID-9606;
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-!- SIMILARITY: BE
EMBL; AF272774; AA
HSSP; P00761; 1AN1
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230; Conserv
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                                          Primates;
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Last annotation update)
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Pred. No. 5.7e
2; Mismatches
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                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                             PRT;
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SEQUENCE FROM N
TISSUE=B-céll;
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527
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240; Conserv
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                                                                                                                                                                                                                                                                             GKGLEWVSAISASGHSTYLADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKD--
MPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK
                    VLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                  GVEVHNAKTKPREEQYNGTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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597 AA; 6
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                                                                                                                                                                                                  -PCPAPELLGGPS-----
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Pred. No. 6.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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.1e-79;
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Search completed: September 12, 2003, 13:03:27 Job time: 85.3475 secs

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9 5	SEQUENCE FROM N.A.
×	MEDLINE=82274238; PubMed=6287432;
í⋝	.E.;
ÄĄ	"The nucleofide sequence of a numan immunogropulify C gammai gene.";
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Đ S	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
×	MEDLINE=71064024; PubMed=5489771;
S S	Cunningham B.A., Rutishauser U., Gall W.E., Gotti:eb P.D., Waxdal M.J., Edelman G.M.:
ij	"The covalent structure of a human gamma G-immuno(lobulin. VII. Amino
ij	
žĤ	Biochemistry 9:3161-31/0(19/0). [3]
õ	SEQUENCE OF 136-329 (EU).
5 5	Bonnott C
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Ĥ	man gamma G-immunoglobulin. 8.
ij	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
ŹĖ	[4]
ξij	UENCE (MYELOMA PROTEIN NIE).
5	Ponsting H. Hilschmann N.;
ij	"The rule of antibody structure. The primary structure of a
Ä	monoclonal IgG1 immunoglobulin (myeloma protein N.e). III. The
4 2	chymotryptic peptides of the complete structure.":
F	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
Ψē	SEOUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
×	131; PubMed=6884994;
Š	N.;
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F	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
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₹ 10	DISULFIDE BONDS.
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ij	"The covalent structure of a human gamma G-immuno; lobulin. X.

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and its complex with fragment B of protein A from Staphylococcus

T aureus at 2.9- and 2.8-A resolution.";

E Biochemistry 20:2361-2370(1981)

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InterPro; IPR003597; Ig_c1.
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"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

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K -> R (IN G1M(3) MARKER).

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D -> E (IN G1M(NON-1) MARKER).

/FTId-VAR_003887.

L -> M (IN G1M(NON-1) MARKER).

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"A note of the amino acid sequence immunoglobulins gamma chains.";
Mol. Immunol. 16:923-925(1979).
                                                                                    REVISIONS HOFMann T.
Stoppini M., Beliotti V., "Characterization of the immunoglobulins.";
                  SEQUENCE OF 1-121 (DOT).
MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A.,
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"The primary structure of a human IgG2 heavy
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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"Linkage and sequence homology of two human immunoglobulin heavy chain constant region genes.";
heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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21-JUL-1986
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MEDLINE-80114419; PubMed-118920;
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21-JUL-1986 (Rel. 01, Last sequence up. 16-OCT-2001 (Rel. 40, Last annotation
                                                                                  Hofmann
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J. Biochem. 57:758-767(1979).
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                                                                       (MAR-1980)
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InterPro; IPR003006; Ig_MHC.
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PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFNWYVDGVEVHNAKTKPREEQFN
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Pink J.R.L., Buttery S.H., de Viles G.M.,
"Human immunoglobulin subclasses. Partial
constant region of a gamma 4 chain.";
Biochem. J. 117:33-47(1970).
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GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
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InterPro; IPR0030906; Ig_MHC.
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MEDLINE-70110015; PubMed-5461106;
Fruchter R.G., Jackson S.A., Mole
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                                                         SEQUENCE OF 88-266 FROM N.A.

MEDLINE-83299917; PubMed-6193512;

MARTHERS C.L., MOOTE K.W., Steinmetz M., Hood L., Knight K.L.;

"Heavy chain genes of rabbit IgG: isolation of a CDNA encoding heavy chain and identification of two genomic C gamma genes."

Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
                                                                                                                              SEQUENCE OF 1-128.

MEDLINB-76135469; PubMed-1243651;

Pratt D.M., Mole L.E.;

"Sequence studies on the constant region immunoglobulin G of different allotype.

Biochem. J. 151:337-349(1975).
                                                                                                                                                                                                            "Nucleotide F-I haplotyp
                                                                                                                                                                                                                                                                              Oryctolagus cuniculus
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; La
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   "Sequence studies immunoglobulin G.
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Chordata; Craniata; Veruchordata; Leporidae; C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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104-THR, AND THE E14 MARKER, 1
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Killander J.
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                     Pfam; PF00047; ig; 2.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                       Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
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Mammalia; Eutheria;
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Cavia porcellus (Guinea pig).
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
                                                                                                                                                                                                                                -i- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM FOOLED SERUM OF 13 INBRED GUINEA PIGS.
                                                                                                                                                                                                                                                                             Biochemistry 10:26-31(1971)
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MEDLINE=71058474;
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Trischmann T.M., Cebra
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and hinge region cyanogen bromide fragments.";
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chemistry 10:9-17(1971).
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A94553; G2GP.
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REVISIONS TO 59-289 (PROTEIN WIS/DIS
MEDLINE-77021516; PubMed-823945;
Wolfenstein-Todel C., Frangione B.,
"The amino acid sequence of 'heavy c
Structure of the Fc fragment of immu
                                                                REVISIONS TO 12-97 (PROTEIN WIS).

MEDLINE-77118561; PubMed-402363;

Michaelsen T.E., Frangione B., Franklin E.C.

"Primary structure of the 'hinge' region of quadruplication of a 15-amino acid residue by Biol. Chem. 252:883-889(1977).
                                                                                                                                         SEQUENCE (DISEASE PROTEIN WIS).

MEDLINE-81021548; PubMed-6774747;

Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;

"Primary structure of human gamma 3 immunoglobulin deletion gamma 3 heavy-chain disease protein Wis.";

Blochemistry 19:4304-4308(1980).
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION NORMALLY PRESENT IN THE HINGE REGION.
MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS T
                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Excupean Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
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                                                                                                                                                                                                                                      Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 74:473-482(1988).
PIR; PS0017; PS0017.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig gamma-1 chain C region Rattus norvegicus (Rat). Eukaryota; Metazoa; Choro Mammalia; Eutheria; Roder
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InterPro; IPR003597;
InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE-89232738;
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                                                                                                                                                                                                                      Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Evolution of the rat
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T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
/FTId=VAR_003894.
MISSING (IN ZUC).
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F -> Y (IN OMM).
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INTERCHAIN
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Best Local Sim
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                        EMBL; J00451; ; NOT_AN
PIR; B02156; G3MSC.
HSSP; P01857; IEC1.
InterPro; IPR007110; Ig
InterPro; IPR003597; Ig
InterPro; IPR003006; Ig
Pfam; PF00047; ig; 3
SMART; SM00407; IGC1; 2
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P22436;
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDIJNE-85027161; PubMed-6092053;

Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;

"Structural analysis of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Creat
01-AUG-1991 (Rel. 19, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrati;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridie;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
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Pred. No. 3
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Best Local
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SEQUENCE FROM N.A.
MEDLINE-80045036; PubMed-115593;
MEDLINE-80045036; PubMed-115593;
Obata M., Yamawaki-Kataoka Y., Kataoka
                                                          Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., (Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.; "Immunoglobulin gamma I heavy chain gene: structural gene cloned in a bacterial plasmid."; Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                 P01868.
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 gamma-1 chain C region secreted for
MEDLINE-80012837; PubMed-113; Rogers J., Clarke P., Salser "Sequence analysis of cloned heavy chain.";
                                                                                                              MEDLINE-80202559; PubMed-6769752;
                                                                                                                       SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                          Mus musculus (Mouse)
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                                                                                                                                                       "Cloning and complete nucleotide gamma 1 chain gene.";
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Immunoglobulin domain; Imn
                                                                                                                                             18:559-568(1979).
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224
329
                            70-322 FROM N.A. (MYELOMA 12837; PubMed=113776;
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113 H
223 C
327 C
36228 MW;
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Pred. No. 7e-7
14; Mismatches
          CDNA
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Sciurognathi;
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                                        PROTEIN
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thi; Muridae; Murinae; Mus
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        part
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                                                                                                                        MOPC
                                        MOPC
         of
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Query Match
Best Local S
Matches 207
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EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PJR; A02159; GIMS.
PDB; 11GC; 03-JUN-95.
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InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 3.
SMART; SM00407; IGC1; 2.
                                                                                       DISULFID
                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 3. PROSITE; PS00290; IG_MHC; 1.
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InterPro; IPR007110; I
                                                                                                                                                                                                                                                                                                                                                PDB; 1IGC; 03-JUN-95.
GlycoSuiteDB; P01868; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Svasti J., Milstein C.; "The disulphide bridges of a mouse immunoglobulin Gl protein."; Biochem. J. 126:837-850(1972).
                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Evolution of immunoglobulin subclasses. murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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                                                                                                                                                                                                                                           Alternative
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[4]
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Name-Secreted;
IsoId-P01868-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Membrane-bound
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             Similarity
  Conservative
                                                                                                                                                                                                                                          splicing;
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            45.5%;
62.3%;
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Score 1145; D
Pred. No. 1.5e
55; Mismatches
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N -> D (IN REF. 3).
; A338812F3D1F2C93 CRC64;
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P20761;
01-FEB-1991 (Rel. 17, Crea
01-FEB-1991 (Rel. 17, Last
15-SEP-2003 (Rel. 42, Last
15-SEP-2003 (Rel. 42, Last
1g gamma-2B chain C region
Rattus norvegicus (Rat).
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DOMAIN 6
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
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InterPro; IPR003597;
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                                                             Local Similarity
les 214; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               e 74:473-482(1988).
SIMILARITY: Contains
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E; PS00290; IG_MHC; 1.
ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
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                                                           Score 1144.5; DB 1; Pred. No. 1.7e-71; 5; Mismatches 68;
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IG-LIKE 2.
IG-LIKE 3.
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ID GCLM_MOUSE
AC P01869;
DT 21-JUL-1986
DT 01-AUG-1991
DT 01-AUG-1991
DT 01-AUG-1991
DT 01-SEP-2003
DE IG gamma-1 conserved reference of the following and partial proc. Natl.
RI Tyler B.M.,
RT Gamma 1 cha.
RI Gell 18:559
RN [2]
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RA Tyler B.M.,
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RT Gamma 1 cha.
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Takahashi N., Mano Y.;
"Cloning and complete nucleotide
gamma 1 chain gene.";
Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                         MEDLINE=82115295; PubM
Rogers J., Choi E., So
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved transmembrane domain.";
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01-AUG-1991 (Rel. 19, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig gamma-1 chain C region, membrane-bound for
                                                                                                                                 "Nucleotide sequences of gene segments encoding n immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                                                                                              SEQUENCE OF 1-44 FROM N.A. MEDLINE=82222190; PubMed=6
                                                                                                                                                                                                                                                                    "Gene segments encoding transmembrane immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 323-366 FROM N.A. MEDLINE=82115295; PubMed=6799207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tyler B.M., Cowman A.F., Gerondakis S.D., "mRNA for surface immunoglobulin gamma cha conserved transmembrane sequence and a 28
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Yamawaki-Kataoka Y., Nakai S., Miyata
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                                                                                                                     ALTERNATIVE PRODUCTS:
                                       Name=Secreted;
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                                                                                               Event=Alternative splicing;
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 sequence=External;
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Pf4am; PF00047; Ig; 3.
SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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                                                                                                  GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS
                                                         EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                   YNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSR
                                                                                                                                                                     --SSVEIFPPKPKDVLTITLTPKVTCVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ
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IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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118-MAR-98.
112-JAN-00.
06-FEB-01.
29-DEC-99.
24-JUL-02.
11-MAY-02.
11-MAY-02.
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                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Cransmembrane; 3D-
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INTERCHAIN
INTERCHAIN
INTERCHAIN
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Pred. No. 4
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CH2.
CH3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    YTOPLASMIC (POTENTIAL)
4CC88343B7A1CE27 CRC6
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HTIW)
HTIW)
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RESULT 12
GC3M_MOUSE
ID GC3M_MOUSE
AC P03987;
DT 23-CCT-1986
DT 01-AUG-1991
DT 01-AUG-1991
DT 15-JUL-1999
DE IG 9amma-3 (OS Mus musculiks)
OC Eukaryota; NOC Eukaryota; NOC Eukaryota; NOC EUKaryota; NOC EUKaryota; EUKaryo
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Best Local S
Matches 213
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SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; J00451; AAB59655.1; -
EMBL; V01556; CAA24767.1; ALT_SEQ.
PIR; A02156; GJMSM.
HSSP; P01857; 1FC1.
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Tucker P.W., Blattner F.R.;
"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-85027161; PubMed-6092053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-OC7-1986 (Rel. 02, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P03987;
23-OCT-1986
                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 328-398 FROM N.A. MEDLINE-84041483; PubMed-6314258;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Komaromy M., Clayton L., Rogers
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                          146 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
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13; Conservative
  TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG
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398
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                                                                                                                                                                      MW.
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CH2.
CH3.
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> F (IN REF. 2).
P -> F (IN REF. 2).
                                                                               Score 1139; D
Pred. No. 5.1e
44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constant region gene.";
                                                                                  ies 68;
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                                                                                                                          Length 398;
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DT 21-JUL
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OC EUKARY
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RN [1]
RN SIKORN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE=81198976; PubMed=6262729;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;
Yamawaki-Kataoka Y., Miyata T., Honjo T.;

"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";

sequence-mediated domain transfer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. (
21-JUL-1986 (Rel. (
15-SEP-2003 (Rel. 4
19 gamma-2A chain (
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21-JUL-1986
21-JUL-1986
15-SEP-2003
                               de Preval C., Fougereau M.;

"Determination of the primary structure of a mouse gamma immunoglobulin. Identification of the disulfide bridges."

Eur. J. Biochem. 30:452-462(1972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-81076554; PubMed-6777755;
MEDLINE-81076554; PubMed-6777755;
MEDLINE-81076554; PubMed-6777755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID-10090;
                                                                                                                                    DISULFIDE BONDS.
MEDLINE=73056887; PubMed=4565406;
                                                                                                                                                                                                              Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amfino-acid sequence of the Fc fragment. Impl for the evolution of immunoglobulin structure and function. J. Biochem. 43:423-435(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                               suggests that exons can be family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-81223894; PubMed-6787604;
Ollo R., Auffray C., Morchamps C., Rougeon F.
"Comparison of mouse immunoglobulin gamma 2a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sikorav J.-L., Auffray C., Rougeon F.;
"Structure of the constant and 3' untranslated
Balb/c gamma 2a heavy chain messenger RNA.";
Nucleic Acids Res. 8:3143-3155(1980).
                                                                                                                                                                                                                                                                                                                                    MYELOMA PROTEIN MOPC 173.
MEDLINE-74175517; PubMed-4831970;
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                           SIMILARITY: Contains
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PDB; 1E4X; 12-JUL-01.
PDB; 1MNU; 06-MAY-99.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PF000407; Ig; 2.
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212; Conserv
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                                                                                    EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
                                                                                                                                                           GGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHRED
                              NWVERNSYSCSVVHEGLHNHHTTKSFSRTPGK
                                                   RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                        EEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKK
                                                                                                                  YNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERIISKPKGSVRAPQVYVLPPPE
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Pred. No. 1.9e
13; Mismatches
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IG-LIKE 2.
IG-LIKE 3.
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B84361C5445A6864 (:RC64;
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SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3

PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brueggemann M., Delmastro-Galfre P., Waldmann H. "Sequence of a rat immunoglobulin gamma 2c heavy region cDNA: extensive homology to mouse gamma 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88166903; PubMed-3127222;
Brueggemann M., Delmastro-Galfre P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
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           SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                            QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                         ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
DSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK
                                        REQMSKNKVSLTCMVTSFYPAS:
                                                   REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                 QLNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYTIPPP
                                                                                                                                                                   GLYTLSSSVTVPSSTWSSOTVTCSVAHPATKSNLIKRIEPR---RPKPRPPTDICSCDDN
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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Rodentia;
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Pred. No. 2.5
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RESULT

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145 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS

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21-JUL-1986
15-SEP-2003
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Dognin M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine chain Fc regions of Igla and Iglb allotypic forms. Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
-!- SUBCELLULAR LOCATION: Secreted (Potential).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schreier P.H., Bothwell A.L.M., Mueller-Hill B., multiple differences between the nucleic acid se IgG2aa and IgG2ab alleles of the mouse.; proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                     SEQUENCE
                                                                                                                                      PROSITE; PS50835; IG_LIKE; PROSITE; PS00290; IG_MHC;
                                                                                                                                                             Pfam; PF00047; ig; SMART; SM00407; IG;
                                                                                                                                                                               InterPro; IPR007110; Ig-like InterPro; IPR003597; Ig_cl. InterPro; IPR003006; Ig_MHC.
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                                                                                                              3D-structure;
                                                                                                                        Immunoglobulin domain; Immunoglobulin C
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-SEP-2003 (Rel. 42, Last annotation updat gamma-2A chain C region secreted form (H
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                                                                                                                                                                                                                   ; 1BOG; 23-MAR-99.
; 1HH6; 26-JAN-01.
; 1HH9; 12-JAN-01.
; 1HI6; 08-FEB-01.
                                                                                                                                                                                                                                                                                                                                               ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF TH FROM BALB/C MICE, AT 15% OF THE POSITIONS.
SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: THE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-Secreted;
                                                                                                                                                                                                                                                                 A02153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Event=Alternative
                                                                                                                                                                                                                                                                           J00479; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note=Probably the major isoform,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IsoId=P01864-1;
                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                  Similarity
                                                  126
234
335
        Conservative
                                                                                                                                                                                                                                                                 G2MSAB
                                                                                                             Repeat.
                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                          IGc1; 2.
                                         98
225
330
36596 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01,
                  44.8%;
61.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                     X
X
        52;
                                                                                                                                               ω.
Pred. No. 2.5c
52; Mismatches
                                                               IG-LIKE
IG-LIKE
                   Score 1126.5;
Pred. No. 2.9e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                     FA3382792CBB13C6 CRC64;
                                                                 ω N F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335
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                                                                                                                                                                                                                                                                                                                                   There are no restrictions ng as its content is in
                                                                                                                         region; Alternative splicing;
                   .9e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (B allele)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                             DB 1;
                                                                                                                                                                                                                                                                                                                          Usage
        70;
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                                                                                                                                                                                                                                                                                                                                                            and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma
        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                      THE
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                              335;
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       Gaps
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	300 VQKSTWERGSLFACSVVHEVLHNHLTTKTISRSLGK 335	300	DЬ
,	::::::::::::::::::::::::::::::	,	!
	439 VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474	439	Qy
KNTATVLDSDGSYFMYSKLR 299	PPPAEEMTKKEFSLTCMITGFLPAEIAVDWTSNGRTEQNYKNTATVLDSDGSYFMYSKLR	240	Db
KTTPPVLDSDGSFFLYSKLT 438	379 PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT	379	Qy
IEKTISKPRGPVRAPQVYVL	180 HREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNRALPSPIEKTISKPRGPVRAPQVYVL 239	180	В
IEKTISKAKGQPREPQVYTL 378	RE	319	Qy
OVQISWEVNNVEVHTAQTQT 179	120 PDLLGGPSVFIFPPKIKDVLMISLSPMVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQT	120	ф
EVKFNWYVDGVEVHNAKTKP 318	259 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKP	259	Qy
RVPITQNPCPPHQRVPPCAA	60 GLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRVPITQNPCPPHQRVPPCAA 119	60	Db
KSCDKTHTCPPCPA 258	_	205	Qy
NSGSLSSGVHTFPALLQ-S	. AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQ-S 59	1	В

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